

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 26, 2005, 11:30:01 ; Search time 24.6 Seconds
(without alignments)
520.089 Million cell updates/sec

Title: US-10-085-612A-1

Perfect score: 18
Sequence: 1 gacaaaggcagacagag 18

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16.4	91.1	29	US-09-144-367-13	Sequence 13, Appl
2	16.4	91.1	1345	US-09-372-339-2	Sequence 2, Appl
3	16	88.9	1345	US-09-144-367-3	Sequence 3, Appl
4	15.4	85.6	19	US-09-144-367-4	Sequence 4, Appl
5	15.4	85.6	45546	US-09-144-053-6	Sequence 6, Appl
6	14.8	82.2	32	US-09-144-367-12	Sequence 12, Appl
7	14.8	82.2	459	US-09-621-976-3153	Sequence 12, Appl
8	14.8	82.2	807	US-08-154-019-28	Sequence 28, Appl
9	14.8	82.2	807	US-08-464-167-28	Sequence 28, Appl
10	14.8	82.2	807	US-08-464-167-28	Sequence 28, Appl
11	14.8	82.2	807	US-09-158-313-28	Sequence 28, Appl
12	14.8	82.2	807	US-08-476-798-28	Sequence 28, Appl
13	14.8	82.2	824	US-08-154-019-29	Sequence 29, Appl
14	14.8	82.2	824	US-08-464-167-29	Sequence 29, Appl
15	14.8	82.2	824	US-08-464-167-29	Sequence 29, Appl
16	14.8	82.2	824	US-09-158-313-29	Sequence 29, Appl
17	14.8	82.2	824	US-08-476-798-29	Sequence 29, Appl
18	14.8	82.2	1057	US-09-716-129-16	Sequence 16, Appl
19	14.8	82.2	1202	US-09-904-615-63	Sequence 63, Appl
20	14.8	82.2	1345	US-09-372-339-1	Sequence 1, Appl
21	14.8	82.2	1452	US-09-904-615-34	Sequence 34, Appl
22	14.8	82.2	1950	US-09-205-258-131	Sequence 131, App
23	14.8	82.2	4523	US-09-472-716-1	Sequence 1, Appl
24	14.8	82.2	4523	US-10-175-158-1	Sequence 1, Appl
25	14.8	82.2	6763	US-08-756-506-23	Sequence 23, Appl
26	14.8	82.2	10807	US-08-206-176-7	Sequence 7, Appl
27	14.8	82.2	10807	US-08-756-506-5	Sequence 5, Appl

28	14.8	82.2	16063	US-09-801-052-3	Sequence 3, Appl
29	14.8	82.2	16063	US-10-020-121-3	Sequence 3, Appl
30	14.8	82.2	29629	US-09-729-995-3	Sequence 3, Appl
31	14.8	82.2	29629	US-10-135-689-3	Sequence 3, Appl
32	14.8	82.2	48974	US-08-920-422-17	Sequence 17, Appl
33	14.8	82.2	66933	US-09-544-398B-11	Sequence 11, Appl
34	14.8	82.2	66933	US-09-543-771-11	Sequence 11, Appl
35	14.8	82.2	72049	US-09-544-398B-9	Sequence 9, Appl
36	14.8	82.2	72049	US-09-543-771-9	Sequence 9, Appl
37	14.8	82.2	118999	US-09-791-105B-32	Sequence 32, Appl
38	14.8	82.2	152331	US-09-128-155-16	Sequence 16, Appl
39	14.8	82.2	176373	US-09-128-155-17	Sequence 17, Appl
40	14.8	82.2	193303	US-09-497-855A-37	Sequence 37, Appl
41	14.8	82.2	193303	US-09-497-855A-44	Sequence 44, Appl
42	14.4	80.0	19	US-09-177-359-37	Sequence 37, Appl
43	14.4	80.0	420	US-09-702-705-1114	Sequence 1114, Ap
44	14.4	80.0	420	US-09-736-457-1114	Sequence 1114, Ap
45	14.4	80.0	420	US-09-614-124B-1114	Sequence 1114, Ap

ALIGNMENTS

```
RESULT 1
US-09-144-367-13/c
; Sequence 13, Application US/09144367
; Patent No. 6432639
; GENERAL INFORMATION:
; APPLICANT: Lichter, Jay
; APPLICANT: Guido, Marco
; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
; FILE REFERENCE: SEO-12P
; CURRENT APPLICATION NUMBER: US/09/144,367
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/058,612
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 29
; TYPE: DNA
; ORGANISM: H. sapiens
US-09-144-367-13

Query Match      91.1%; Score 16.4; DB 4; Length 29;
Best Local Similarity 94.4%; Pred. No. 41;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy      1 GACAAAGGCAGACAGAG 18
Db      24 GACAAAGGCAGACAGAG 7

RESULT 2
US-09-372-339-2
; Sequence 2, Application US/09372339
; Patent No. 6174684
; GENERAL INFORMATION:
; APPLICANT: Rebbeck, Timothy
; APPLICANT: Felix, Carolyn
; TITLE OF INVENTION: CYP3A4 NFE Variant and Methods of Use Therefor
; FILE REFERENCE: PENN-0695
; CURRENT APPLICATION NUMBER: US/09/372,339
; CURRENT FILING DATE: 1999-08-11
; EARLIER APPLICATION NUMBER: 60/096,586
; EARLIER FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-372-339-2
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Query Match 91.1%; Score 16.4; DB 3; Length 1345;
Best Local Similarity 94.4%; Pred. No. 58;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GACAAGGCGACAGACAG 18
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DB 806 GACAAGGCGACAGACAG 823

RESULT 3

US-09-144-367-3
; Sequence 3, Application US/09144367
; Patent No. 6432639
; GENERAL INFORMATION:
; APPLICANT: Lichter, Jay
; APPLICANT: Guido, Marco
; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
; FILE REFERENCE: SEQ-12P
; CURRENT APPLICATION NUMBER: US/09/144,367
; CURRENT FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/058,612
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: Other
; LOCATION: (0)...(0)
US-09-144-367-3

Query Match 88.9%; Score 16; DB 4; Length 1345;
Best Local Similarity 88.9%; Pred. No. 89;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GACAAGGCGACAGACAG 18
|||||
DB 806 GACAAGGCGACAGACAG 823

RESULT 4

US-09-144-367-44
; Sequence 44, Application US/09144367
; Patent No. 6432639
; GENERAL INFORMATION:
; APPLICANT: Lichter, Jay
; APPLICANT: Guido, Marco
; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
; FILE REFERENCE: SEQ-12P
; CURRENT APPLICATION NUMBER: US/09/144,367
; CURRENT FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/058,612
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 19
; TYPE: DNA
; ORGANISM: H. sapiens
US-09-144-367-44

Query Match 85.6%; Score 15.4; DB 4; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ACAAGGCGACAGACAG 18
|||||
DB 1 ACAAGGCGACAGACAG 17

RESULT 5
US-09-146-053-6
; Sequence 6, Application US/09146053A
; Patent No. 6399349
; GENERAL INFORMATION:
; APPLICANT: Ryan, James W.
; APPLICANT: Sprinkle, Terry Joe Curtis
; APPLICANT: Venema, Richard C.
; TITLE OF INVENTION: Human Aminopeptidase P Gene
; FILE REFERENCE: MCG103
; CURRENT APPLICATION NUMBER: US/09/146,053A
; CURRENT FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/057,854
; EARLIER FILING DATE: 1997-09-02
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 45546
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-146-053-6

Query Match 85.6%; Score 15.4; DB 3; Length 45546;
Best Local Similarity 94.1%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GACAAGGCGACAGACA 17
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DB 565 GACAAGGCGACAGACA 581

RESULT 6

US-09-144-367-12/c
; Sequence 12, Application US/09144367
; Patent No. 6432639
; GENERAL INFORMATION:
; APPLICANT: Lichter, Jay
; APPLICANT: Guido, Marco
; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
; FILE REFERENCE: SEQ-12P
; CURRENT APPLICATION NUMBER: US/09/144,367
; CURRENT FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/058,612
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 32
; TYPE: DNA
; ORGANISM: H. sapiens
US-09-144-367-12

Query Match 82.2%; Score 14.8; DB 4; Length 32;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GACAAGGCGACAGACAG 18
|||||
DB 27 GACAAGGCGACAGACAG 10

RESULT 7

US-09-621-976-3153
; Sequence 3153, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET 054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO: 3153
LENGTH: 459
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 150..329
US-09-621-976-3153

Query Match 82.2%; Score 14.8; DB 4; Length 459;
Best Local Similarity 88.9%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GACACGGCGCAGACAGAG 18
DB 198 GACACGGCGCTGACAGAG 215

RESULT 8
US-08-154-019-28/c
Sequence 28, Application US/08154019
Patent No. 5633076
GENERAL INFORMATION:
APPLICANT: Deboer, Herman A.
APPLICANT: Strijker, Rein
APPLICANT: Heyneker, Herbert L.
APPLICANT: Platenburg, Gerald
APPLICANT: Lee, Sang He
APPLICANT: Pieper, Frank
APPLICANT: Krimpenfort, Paul J.A.
TITLE OF INVENTION: Production of Recombinant Polypeptides
TITLE OF INVENTION: by Bovine Species and Transgenic Methods
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/154,019
FILING DATE: 16-NOV-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/461,333
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: US 08/077,788
FILING DATE: 15-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/444,745
FILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Liebescheutz, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16994-003123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:
LENGTH: 807 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-154-019-28

Query Match 82.2%; Score 14.8; DB 1; Length 807;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GACACGGCGCAGACAGAG 18
DB 411 GACACGACAGCTGACAGAG 394

RESULT 9
US-08-461-333-28/c
Sequence 28, Application US/08461333
Patent No. 5741957
GENERAL INFORMATION:
APPLICANT: Deboer, Herman A.
APPLICANT: Strijker, Rein
APPLICANT: Heyneker, Herbert L.
APPLICANT: Platenburg, Gerald
APPLICANT: Lee, Sang He
APPLICANT: Pieper, Frank
APPLICANT: Krimpenfort, Paul J.A.
TITLE OF INVENTION: Production of Recombinant Polypeptides
TITLE OF INVENTION: by Bovine Species and Transgenic Methods
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,333
FILING DATE: 05-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,788
FILING DATE: 15-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/444,745
FILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Liebescheutz, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16994-003123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 807 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-461-333-28

Query Match 82.2%; Score 14.8; DB 1; Length 807;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GACAAAGGCGACGACGAG 18
Db 411 GACAAGGACAGCTCAGAG 394

RESULT 10
US-08-464-167-28/c
Sequence 28, Application US/08464167
Patent No. 6013857

GENERAL INFORMATION:
APPLICANT: Deboer, Herman A.
APPLICANT: Strijker, Rein
APPLICANT: Heyneker, Herbert L.
APPLICANT: Platenburg, Gerald
APPLICANT: Lee, Sang He
APPLICANT: Pieper, Frank
APPLICANT: Krimpenfort, Paul J.A.
TITLE OF INVENTION: Production of Recombinant Polypeptides
TITLE OF INVENTION: by Bovine Species and Transgenic Methods
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,167
FILING DATE: 05-JUN-1995
CLASSIFICATION: 800

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,788
FILING DATE: 15-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/444,745
FILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Liebescheutz, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16994-003124
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043

INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 807 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-464-167-28

Query Match 82.2%; Score 14.8; DB 3; Length 807;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GACAAAGGCGACGACGAG 18
Db 411 GACAAGGACAGCTCAGAG 394

RESULT 11
US-09-158-313-28/c
Sequence 28, Application US/09158313
Patent No. 6066725

GENERAL INFORMATION:
APPLICANT: Deboer, Herman A.
APPLICANT: Strijker, Rein
APPLICANT: Heyneker, Herbert L.
APPLICANT: Platenburg, Gerald
APPLICANT: Lee, Sang He
APPLICANT: Pieper, Frank
APPLICANT: Krimpenfort, Paul J.A.
TITLE OF INVENTION: Production of Recombinant Polypeptides
TITLE OF INVENTION: by Bovine Species and Transgenic Methods
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/158,313
FILING DATE: 08/476,798

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,798
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/444,745
FILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Liebescheutz, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16994-003125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043

INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 807 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-158-313-28

Query Match 82.2%; Score 14.8; DB 3; Length 807;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GACAAAGGCGACGACGAG 18
Db 411 GACAAGGACAGCTCAGAG 394

RESULT 12
US-08-476-798-28/c
; Sequence 28, Application US/08476798
; Patent No. 6140552
; GENERAL INFORMATION:
; APPLICANT: Deboer, Herman A.
; APPLICANT: Strijker, Rein
; APPLICANT: Heyneker, Herbert L.
; APPLICANT: Platenburg, Gerald
; APPLICANT: Lee, Sang He
; APPLICANT: Pieper, Frank
; APPLICANT: Krumpfort, Paul J.A.
; TITLE OF INVENTION: Production of Recombinant Polypeptides
; TITLE OF INVENTION: by Bovine Species and Transgenic Methods
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Stewart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,798
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,788
; FILING DATE: 15-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/895,956
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/619,131
; FILING DATE: 27-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/444,745
; FILING DATE: 01-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschultz, Joe O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 16994-003125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 807 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-476-798-28

Query Match 82.2%; Score 14.8; DB 3; Length 807;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GACAAGGCGACGACGAG 18
|||
Db 411 GACAAGGCGACGTCGAG 394

RESULT 13
US-08-154-019-29/c
; Sequence 29, Application US/08154019

; Patent No. 5633076
; GENERAL INFORMATION:
; APPLICANT: Deboer, Herman A.
; APPLICANT: Strijker, Rein
; APPLICANT: Heyneker, Herbert L.
; APPLICANT: Platenburg, Gerald
; APPLICANT: Lee, Sang He
; APPLICANT: Pieper, Frank
; APPLICANT: Krumpfort, Paul J.A.
; TITLE OF INVENTION: Production of Recombinant Polypeptides
; TITLE OF INVENTION: by Bovine Species and Transgenic Methods
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Stewart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/154,019
; FILING DATE: 16-NOV-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/461,333
; FILING DATE: 05-JUN-1995
; APPLICATION NUMBER: US 08/077,788
; FILING DATE: 15-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/895,956
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/619,131
; FILING DATE: 27-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/444,745
; FILING DATE: 01-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschultz, Joe O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 16994-003123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 824 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-154-019-29

Query Match 82.2%; Score 14.8; DB 1; Length 824;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GACAAGGCGACGACGAG 18
|||
Db 417 GACAAGGCGACGTCGAG 400

RESULT 14
US-08-461-333-29/c
; Sequence 29, Application US/08461333
; Patent No. 5741957
; GENERAL INFORMATION:
; APPLICANT: Deboer, Herman A.

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; APPLICANT: Strijker, Rein
; APPLICANT: Heyneker, Herbert L.
; APPLICANT: Platenburg, Gerald
; APPLICANT: Lee, Sang He
; APPLICANT: Pieper, Frank
; APPLICANT: Krampenfort, Paul J.A.
; TITLE OF INVENTION: Production of Recombinant Polypeptides
; TITLE OF INVENTION: by Bovine Species and Transgenic Methods
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Stewart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,333
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,788
; FILING DATE: 15-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/895,956
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/619,131
; FILING DATE: 27-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/444,745
; FILING DATE: 01-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebescheutz, Joe O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 16994-003123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 824 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-461-333-29

Query Match      82.2%; Score 14.8; DB 1; Length 824;
Best Local Similarity 86.9%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GACAAGGCGACGACGAG 18
Db      417 GACAAGGACAGGTCTCAGG 400

RESULT 15
; US-08-464-167-29/c
; Sequence 29, Application US/08464167
; Patent No. 6013857
; GENERAL INFORMATION:
; APPLICANT: Deboer, Herman A.
; APPLICANT: Strijker, Rein
; APPLICANT: Heyneker, Herbert L.
; APPLICANT: Platenburg, Gerald
; APPLICANT: Lee, Sang He
; APPLICANT: Pieper, Frank
```

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; APPLICANT: Krampenfort, Paul J.A.
; TITLE OF INVENTION: Production of Recombinant Polypeptides
; TITLE OF INVENTION: by Bovine Species and Transgenic Methods
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Stewart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,167
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,788
; FILING DATE: 15-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/895,956
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/619,131
; FILING DATE: 27-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/444,745
; FILING DATE: 01-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebescheutz, Joe O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 16994-003124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 824 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-464-167-29

Query Match      82.2%; Score 14.8; DB 3; Length 824;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db      417 GACAAGGACAGGTCTCAGG 400
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Search completed: January 26, 2005, 13:15:19
Job time : 25.725 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 26, 2005, 13:15:32 : Search time 127.6 Seconds
(without alignments)
810.549 Million cell updates/sec

Title: US-10-085-612A-1

Perfect score: 18

Sequence: 1 gacaaaggcagacagag 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 287294193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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- 11: /cgn2_6/ptodata/1/pubpna/US09C_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	US-10-085-612-1	Sequence 1, Appl1
2	16.4	91.1	229	US-10-146-575-13	Sequence 13, Appl1
3	16.4	91.1	529	US-10-027-632-106890	Sequence 106890,
4	16.4	91.1	529	US-10-027-632-106890	Sequence 106890,
5	16.4	91.1	714	US-10-027-632-25159	Sequence 25159, A
6	16.4	91.1	714	US-10-027-632-25159	Sequence 25159, A
7	16.4	91.1	1530	US-10-198-846-10454	Sequence 10454, A
8	16.4	91.1	24295	US-10-317-277A-4	Sequence 4, Appl1
9	16.4	91.1	25543	US-10-087-192-805	Sequence 805, App
10	16.4	91.1	34455	US-10-087-192-1915	Sequence 1915, App
11	16.4	91.1	71251	US-10-087-192-355	Sequence 355, App
12	16.4	91.1	73771	US-10-087-192-1636	Sequence 1636, App

13	16.4	91.1	119596	US-10-270-336-3	Sequence 3, Appl1
14	16.4	91.1	172637	US-09-805-458A-3	Sequence 3, Appl1
15	16.4	91.1	227961	US-10-433-580-2	Sequence 2, Appl1
16	16.4	88.9	41	US-10-035-833A-1329	Sequence 1329, App
17	16.4	88.9	41	US-10-035-833A-7586	Sequence 7586, App
18	16.4	88.9	339	US-10-425-115-69563	Sequence 69563, A
19	16.4	88.9	745	US-10-027-632-166368	Sequence 166368,
20	16.4	88.9	745	US-10-027-632-166368	Sequence 166368,
21	16.4	88.9	774	US-10-767-701-14922	Sequence 14922, A
22	16.4	88.9	1345	US-09-943-115A-1	Sequence 1, Appl1
23	16.4	88.9	1345	US-10-146-575-3	Sequence 3, Appl1
24	16.4	88.9	1345	US-10-085-612-3	Sequence 3, Appl1
25	16.4	88.9	2270	US-10-177-917-1	Sequence 1, Appl1
26	16.4	88.9	3881	US-09-948-820-20	Sequence 20, Appl1
27	16.4	88.9	3881	US-10-613-076-20	Sequence 20, Appl1
28	16.4	88.9	88493	US-10-322-281-703	Sequence 703, App
29	15.4	85.6	19	US-09-943-115A-3	Sequence 3, Appl1
30	15.4	85.6	19	US-10-146-575-44	Sequence 44, Appl1
31	15.4	85.6	299	US-09-783-590-3955	Sequence 3955, App
32	15.4	85.6	314	US-10-437-963-49508	Sequence 49508, A
33	15.4	85.6	314	US-10-425-115-40247	Sequence 40247, A
34	15.4	85.6	341	US-10-437-963-19690	Sequence 19690, A
35	15.4	85.6	361	US-10-424-599-6641	Sequence 6641, App
36	15.4	85.6	514	US-10-425-115-105065	Sequence 105065,
37	15.4	85.6	591	US-10-027-632-286257	Sequence 286257,
38	15.4	85.6	591	US-10-027-632-321713	Sequence 321713,
39	15.4	85.6	592	US-10-027-632-321714	Sequence 321714,
40	15.4	85.6	592	US-10-027-632-321714	Sequence 321714,
41	15.4	85.6	592	US-10-027-632-321713	Sequence 321713,
42	15.4	85.6	592	US-10-027-632-321714	Sequence 321714,
43	15.4	85.6	618	US-10-437-963-10910	Sequence 10910, A
44	15.4	85.6	618	US-10-027-632-105305	Sequence 105305,
45	15.4	85.6	618	US-10-027-632-105305	Sequence 105305,

ALIGNMENTS

RESULT 1
US-10-085-612-1
Sequence 1, Application US/10085612
Publication No. US20030096251A1
GENERAL INFORMATION:
APPLICANT: Guida, Marco
APPLICANT: Hall, Jeff
APPLICANT: Petros, William
APPLICANT: Vredenburg, James
APPLICANT: Colvin, Oliver
APPLICANT: Marks, Jeffrey
TITLE OF INVENTION: Methods for Evaluating the Ability to Metabolize Pharmaceuticals
FILE REFERENCE: 4389-5-CI
CURRENT APPLICATION NUMBER: US/10/085,612
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 09/144,367
PRIOR FILING DATE: 1998-08-31
PRIOR APPLICATION NUMBER: 60/271,630
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1:
LENGTH: 18
TYPE: DNA
ORGANISM: Homo sapiens
US-10-085-612-1
Query Match 100.0%; Score 18; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 18; Conservative 0; Mismatches 0; Indels 0;
Gy 1 GACAAAGGCAGACAGAG 18
Db 1 GACAAAGGCAGACAGAG 18

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RESULT 2
US-10-146-575-13/c
; Sequence 13, Application US/10146575
; Publication No. US20030059800A1
; GENERAL INFORMATION:
; APPLICANT: Lichter, Jay
; APPLICANT: Guido, Marco
; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
; FILE REFERENCE: SEQ-12P
; CURRENT APPLICATION NUMBER: US/10/146,575
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US/09/144,367
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 29
; TYPE: DNA
; ORGANISM: H. sapiens
US-10-146-575-13
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Best Local Similarity 94.4%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy      1 GACAAGGCGACGACGAG 18
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Db      24 GACAAGGCGACGACGAG 7
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RESULT 3
US-10-027-632-106890/c
; Sequence 106890, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 106890
; LENGTH: 529
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-106890
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Best Local Similarity 94.4%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy      1 GACAAGGCGACGACGAG 18
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Db      170 GTCAGGCGACGACGAG 153
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RESULT 4
US-10-027-632-106890/c
; Sequence 106890, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; APPLICANT: Guido, Marco
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 106890
; LENGTH: 529
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-106890
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Best Local Similarity 94.4%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy      1 GACAAGGCGACGACGAG 18
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Db      170 GTCAGGCGACGACGAG 153
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RESULT 5
US-10-027-632-25159
; Sequence 25159, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25159
; LENGTH: 714
; TYPE: DNA
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ORGANISM: Human
US-10-027-632-25159

Query Match 91.1%; Score 16.4; DB 13; Length 714;
Best Local Similarity 94.4%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GACAGGGCAGACAGAG 18
DB 361 GTCAGGGCAGACAGAG 378

RESULT 6
US-10-027-632-25159

Sequence 25159, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

PRIOR FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 25159

LENGTH: 714

TYPE: DNA

ORGANISM: Human

US-10-027-632-25159

Query Match 91.1%; Score 16.4; DB 15; Length 714;
Best Local Similarity 94.4%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GACAGGGCAGACAGAG 18
DB 361 GTCAGGGCAGACAGAG 378

RESULT 7
US-10-198-846-10434

Sequence 10434, Application US/10198846

Publication No. US2003009974A1

GENERAL INFORMATION:

APPLICANT: Lillie, James

APPLICANT: Xu, Yongyao

APPLICANT: Wang, Youzhen

APPLICANT: Steinmann, Kathleen

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS

FILE REFERENCE: MRI-049

CURRENT APPLICATION NUMBER: US/10/198,846

PRIOR FILING DATE: 2002-07-18

PRIOR APPLICATION NUMBER: 60/306,220

NUMBER OF SEQ ID NOS: 14084

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 10434

LENGTH: 1530

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc_feature

LOCATION: 897, 1528, 1529, 1530

OTHER INFORMATION: n = A,T,C or G

US-10-198-846-10434

Query Match 91.1%; Score 16.4; DB 14; Length 1530;
Best Local Similarity 94.4%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GACAGGGCAGACAGAG 18
DB 997 GACAGGGCAGACAGAG 1014

RESULT 8
US-10-317-277A-4/C

Sequence 4, Application US/10317277A

Publication No. US20040110159A1

GENERAL INFORMATION:

APPLICANT: Dobie, Kenneth W.

TITLE OF INVENTION: Modulation of Estrogen-Responsive Finger Protein Expression

FILE REFERENCE: RPS-0473

CURRENT APPLICATION NUMBER: US/10/317,277A

PRIOR FILING DATE: 2002-12-10

NUMBER OF SEQ ID NOS: 168

SOFTWARE: PatentIn version 3.2

SEQ ID NO 4

LENGTH: 24295

TYPE: DNA

ORGANISM: Homo sapiens

US-10-317-277A-4

Query Match 91.1%; Score 16.4; DB 17; Length 24295;
Best Local Similarity 94.4%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GACAGGGCAGACAGAG 18
DB 20551 GTCAGGGCAGACAGAG 20534

RESULT 9
US-10-087-192-805

Sequence 805, Application US/10087192

Publication No. US20020182586A1

GENERAL INFORMATION:

APPLICANT: Morris, David W.

APPLICANT: Engelhard, Eric K.

TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR

FILE REFERENCE: 529452000122

CURRENT APPLICATION NUMBER: US/10/087,192

PRIOR FILING DATE: 2002-03-01

PRIOR APPLICATION NUMBER: US 09/747,377

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: US 09/738,586

PRIOR FILING DATE: 2001-03-02

NUMBER OF SEQ ID NOS: 2059

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 805

LENGTH: 25543

TYPE: DNA

ORGANISM: Mus musculus

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(25543)

OTHER INFORMATION: n = A,T,C or G

US-10-087-192-805

Query Match 91.1%; Score 16.4; DB 13; Length 25543;
Best Local Similarity 94.4%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GACAAAGGCGACAGAG 18
Db 6541 GACAAAGGCGACAGAG 6558

RESULT 10

US-10-087-192-1915
; Sequence 1915, Application US/10087192
; Publication No. US20020182586a1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1915
; LENGTH: 34455
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1) -(34455)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-1915

Query Match 91.1%; Score 16.4; DB 13; Length 34455;
Best Local Similarity 94.4%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GACAAAGGCGACAGAG 18
Db 2799 GACAAAGGCGACAGAG 2816

RESULT 11

US-10-087-192-355/c
; Sequence 355, Application US/10087192
; Publication No. US20020182586a1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 355
; LENGTH: 71251
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1) -(71251)
; OTHER INFORMATION: n = A,T,C or G

US-10-087-192-355

Query Match 91.1%; Score 16.4; DB 13; Length 71251;
Best Local Similarity 94.4%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GACAAAGGCGACAGAG 18
Db 43322 GACAAAGGCGACAGAG 43305

RESULT 12

US-10-087-192-1636/c
; Sequence 1636, Application US/10087192
; Publication No. US20020182586a1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1636
; LENGTH: 73771
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1) -(73771)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-1636

Query Match 91.1%; Score 16.4; DB 13; Length 73771;
Best Local Similarity 94.4%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GACAAAGGCGACAGAG 18
Db 66831 GACAAAGGCGACAGAG 66814

RESULT 13

US-10-270-336-3
; Sequence 3, Application US/10270336
; Publication No. US20030074678A1
; GENERAL INFORMATION:
; APPLICANT: ZHU, ShiaoPing et al.
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; FILE REFERENCE: C0001146CON
; CURRENT APPLICATION NUMBER: US/10/270,336
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/270,873
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 119596
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1) -(119596)
; OTHER INFORMATION: n = A,T,C or G
US-10-270-336-3

Query Match 91.1%; Score 16.4; DB 14; Length 119596;
Best Local Similarity 94.4%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GACAGGGCAGACAGAG 18
DB 63483 GACAGGGCAGACAGAG 63500

RESULT 14
US-09-805-458A-3
Sequence 3, Application US/09805458A
Patent No. US20020042100A1
GENERAL INFORMATION:
APPLICANT: YAN, Chunhua et al
TITLE OF INVENTION: ISOLATED HUMAN ION CHANNEL PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN ION CHANNEL PROTEINS,
FILE REFERENCE: CL000722
CURRENT APPLICATION NUMBER: US/09/805,458A
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 172637
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(172637)
OTHER INFORMATION: n = A, T, C or G
US-09-805-458A-3

Query Match 91.1%; Score 16.4; DB 9; Length 172637;
Best Local Similarity 94.4%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GACAGGGCAGACAGAG 18
DB 95503 GACAGGGCAGACAGAG 95520

RESULT 15
US-10-433-580-2
Sequence 2, Application US/10433580
Publication No. US20040091497A1
GENERAL INFORMATION:
APPLICANT: GENSET
TITLE OF INVENTION: SCHIZOPHRENIA RELATED VOLTAGE-GATED ION CHANNEL GENE AND PROTEIN
FILE REFERENCE: 93.WOI
CURRENT APPLICATION NUMBER: US/10/433,580
CURRENT FILING DATE: 2003-06-04
PRIOR APPLICATION NUMBER: US 60/251,317
PRIOR FILING DATE: 2000-12-05
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patent.pm
SEQ ID NO 2
LENGTH: 237961
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: exon
LOCATION: 43726..43868
OTHER INFORMATION: exon 8
FEATURE:
NAME/KEY: exon
LOCATION: 43998..44102
OTHER INFORMATION: exon 9
FEATURE:
NAME/KEY: exon
LOCATION: 52093..52179
OTHER INFORMATION: exon 10

FEATURE:
NAME/KEY: exon
LOCATION: 77568..77699
OTHER INFORMATION: exon 11
FEATURE:
NAME/KEY: exon
LOCATION: 98226..98393
OTHER INFORMATION: exon 12
FEATURE:
NAME/KEY: exon
LOCATION: 106567..106758
OTHER INFORMATION: exon 13
FEATURE:
NAME/KEY: exon
LOCATION: 144109..144246
OTHER INFORMATION: exon 14
FEATURE:
NAME/KEY: exon
LOCATION: 159794..159868
OTHER INFORMATION: exon 15
FEATURE:
NAME/KEY: exon
LOCATION: 191292..191428
OTHER INFORMATION: exon 16
FEATURE:
NAME/KEY: exon
LOCATION: 192867..193108
OTHER INFORMATION: exon 17
FEATURE:
NAME/KEY: exon
LOCATION: 211540..211613
OTHER INFORMATION: exon 18
FEATURE:
NAME/KEY: exon
LOCATION: 225006..225107
OTHER INFORMATION: exon 19
FEATURE:
NAME/KEY: exon
LOCATION: 225544..225613
OTHER INFORMATION: exon 20
FEATURE:
NAME/KEY: exon
LOCATION: 228450..228541
OTHER INFORMATION: exon 21
FEATURE:
NAME/KEY: exon
LOCATION: 228630..228752
OTHER INFORMATION: exon 22
FEATURE:
NAME/KEY: exon
LOCATION: 231289..231345
OTHER INFORMATION: exon 23
FEATURE:
NAME/KEY: exon
LOCATION: 231589..231709
OTHER INFORMATION: exon 24
FEATURE:
NAME/KEY: exon
LOCATION: 231813..231944
OTHER INFORMATION: exon 25
FEATURE:
NAME/KEY: exon
LOCATION: 232800..233067
OTHER INFORMATION: exon 26
FEATURE:
NAME/KEY: exon
LOCATION: 235355..235459
OTHER INFORMATION: exon 27
FEATURE:
NAME/KEY: allele
LOCATION: 51090
OTHER INFORMATION: 99-79335-60 : polymorphic base C or T
FEATURE:

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: NAME/KEY: allele
: LOCATION: 61293
: OTHER INFORMATION: 99-79336-369 : polymorphic base A or G
: FEATURE:
: NAME/KEY: allele
: LOCATION: 80602
: OTHER INFORMATION: 99-79338-332 : polymorphic base C or T
: FEATURE:
: NAME/KEY: allele
: LOCATION: 100485
: OTHER INFORMATION: 99-79314-201 : polymorphic base G or T
: FEATURE:
: NAME/KEY: allele
: LOCATION: 100509
: OTHER INFORMATION: 99-79314-225 : polymorphic base A or G
: FEATURE:
: NAME/KEY: allele
: LOCATION: 106725
: OTHER INFORMATION: 99-79316-158 : polymorphic base C or T
: FEATURE:
: NAME/KEY: allele
: LOCATION: 166087
: OTHER INFORMATION: 99-79322-224 : polymorphic base G or T
: FEATURE:
: NAME/KEY: allele
: LOCATION: 166336
: OTHER INFORMATION: 99-79322-473 : polymorphic base A or G
: FEATURE:
: NAME/KEY: allele
: LOCATION: 235894
: OTHER INFORMATION: 99-79306-182 : polymorphic base C or T
: FEATURE:
: NAME/KEY: primer_bind
: LOCATION: 51031..51051
: OTHER INFORMATION: 99-79335.pu
: FEATURE:
: NAME/KEY: primer_bind
: LOCATION: 51539..51559
: OTHER INFORMATION: 99-79335.rp complement
: FEATURE:
: NAME/KEY: primer_bind
: LOCATION: 60925..60945
: OTHER INFORMATION: 99-79336.pu
: FEATURE:
: NAME/KEY: primer_bind
: LOCATION: 61354..61374
: OTHER INFORMATION: 99-79336.rp complement
: FEATURE:
: NAME/KEY: primer_bind
: LOCATION: 80271..80290
: OTHER INFORMATION: 99-79338.pu
: FEATURE:
: NAME/KEY: primer_bind
: LOCATION: 80700..80720
: OTHER INFORMATION: 99-79338.rp complement
: FEATURE:
: NAME/KEY: primer_bind
: LOCATION: 91037..91056
: OTHER INFORMATION: 99-79339.pu
: FEATURE:
: NAME/KEY: primer_bind
: LOCATION: 91466..91486
: OTHER INFORMATION: 99-79339.rp complement
: FEATURE:
: NAME/KEY: primer_bind
: LOCATION: 100285..100305
: OTHER INFORMATION: 99-79314.pu
: FEATURE:
: NAME/KEY: primer_bind
: LOCATION: 100764..100784
: OTHER INFORMATION: 99-79314.rp complement
: FEATURE:
: NAME/KEY: primer_bind

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: LOCATION: 106568..106585
: OTHER INFORMATION: 99-79316.pu
: FEATURE:
: NAME/KEY: primer_bind
: LOCATION: 107000..107020
: OTHER INFORMATION: 99-79316.rp complement
: FEATURE:
: NAME/KEY: primer_bind
: LOCATION: 165864..165884
: OTHER INFORMATION: 99-79322.pu
: FEATURE:
: NAME/KEY: primer_bind
: LOCATION: 166381..166401
: OTHER INFORMATION: 99-79322.rp complement
: FEATURE:
: NAME/KEY: primer_bind
: LOCATION: 235713..235732
: OTHER INFORMATION: 99-79306.pu
: FEATURE:
: NAME/KEY: primer_bind
: LOCATION: 236190..236210
: OTHER INFORMATION: 99-79306.rp complement
: FEATURE:
: NAME/KEY: primer_bind
: LOCATION: 51071..51089
: OTHER INFORMATION: 99-79335-60.mis

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Query Match          91.1%; Score 16.4; DB 16; Length 237961;
Best Local Similarity 94.4%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GACAAAGGCGACGACGAG 18
Db      29559 GACAAAGGCGACGACGAG 29576

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Search completed: January 26, 2005, 18:15:43
 Job time : 129.6 secs

Query Match 67.1%; Score 22.8; DB 3; Length 1345;
Best Local Similarity 92.3%; Pred. No. 6.7;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TGGTACTGGCTGCAGCTGCAGCCCCG 34
Db 1035 TGGTACTGGCTGCAGCTGCAGCCCCG 1060

RESULT 3

US-09-144-367-3
; Sequence 3, Application US/09144367
; Patent No. 6432639
; GENERAL INFORMATION:
; APPLICANT: Lichter, Jay
; APPLICANT: Guido, Marco
; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
; FILE REFERENCE: SEQ-12P
; CURRENT APPLICATION NUMBER: US/09/144,367
; CURRENT FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/058,612
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: Other
; LOCATION: (0)...(0)
US-09-144-367-3

Query Match 67.1%; Score 22.8; DB 4; Length 1345;
Best Local Similarity 92.3%; Pred. No. 6.7;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TGGTACTGGCTGCAGCTGCAGCCCCG 34
Db 1035 TGGTACTGGCTGCAGCTGCAGCCCCG 1060

RESULT 4

US-09-489-039A-2633/C
; Sequence 2633, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 2633
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-2633

Query Match 61.2%; Score 20.8; DB 4; Length 1023;
Best Local Similarity 78.1%; Pred. No. 38;
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 3 ATTCTTGTACTGCTGCAGCTGCAGCCCCG 34
Db 477 ATTATGGCTACTGTCCGCGACATCAACCCCG 446

RESULT 5

US-09-270-767-6152
; Sequence 6152, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6152
; LENGTH: 445
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: n means any nucleotide
US-09-270-767-6152

Query Match 60.6%; Score 20.6; DB 4; Length 445;
Best Local Similarity 85.2%; Pred. No. 40;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 8 TTGCTACTGGCTGCAGCTGCAGCCCCG 34
Db 373 TCGCTACGAGCTGCAGCTGCAGCACC 399

RESULT 6

US-09-270-767-21434
; Sequence 21434, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21434
; LENGTH: 445
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: n means any nucleotide
US-09-270-767-21434

Query Match 60.6%; Score 20.6; DB 4; Length 445;
Best Local Similarity 85.2%; Pred. No. 40;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 8 TTGCTACTGGCTGCAGCTGCAGCCCCG 34
Db 373 TCGCTACGAGCTGCAGCTGCAGCACC 399

RESULT 7

US-09-394-142B-23/C
; Sequence 23, Application US/09394142B
; Patent No. 6696558
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Takayama, Shinichi
; TITLE OF INVENTION: No. 666558e1 BAG Proteins and Nucleic Acid Molecules Encoding
; FILE REFERENCE: P-LJ 3737
; CURRENT APPLICATION NUMBER: US/09/394,142B
; CURRENT FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: 09/150,489
; PRIOR FILING DATE: 1998-09-09
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0

APPLICANT: NAHUM SONENBERG
ARNIM PAUSE
JOE B. HARFORD
VINCENT J. MILES

TITLE OF INVENTION: METHODS FOR TREATING
HORMONE DISORDERS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/593,483
FILING DATE: 14-Jun-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/294,143
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 202/060
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-593-483-1

Query Match 58.8%; Score 20; DB 4; Length 357;
Best Local Similarity 82.1%; Pred. No. 65;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 6 CTTTGCTACTGGCTGCAGCTGCAGCCCC 33
DB 35 CTTGGGGCTGGCTGCAGCTGCCTGCCCC 8

RESULT 11
US-09-023-655-1445/c
Sequence 1445, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 845-4166
TELEFAX: (650) 845-0555
INFORMATION FOR SEQ ID NO: 1445:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 9561629
US-09-023-655-1445

Query Match 58.8%; Score 20; DB 4; Length 357;
Best Local Similarity 82.1%; Pred. No. 65;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 6 CTTTGCTACTGGCTGCAGCTGCAGCCCC 33
DB 35 CTTGGGGCTGGCTGCAGCTGCCTGCCCC 8

RESULT 12
US-08-294-143-3/c
Sequence 3, Application US/08294143
Patent No. 5874231
GENERAL INFORMATION:
APPLICANT: NAHUM SONENBERG
APPLICANT: ARNIM PAUSE
APPLICANT: JOE B. HARFORD
APPLICANT: VINCENT J. MILES
TITLE OF INVENTION: METHODS FOR TREATING
TITLE OF INVENTION: HORMONE DISORDERS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/294,143
FILING DATE: August 22, 1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 202/060
TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 829 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-294-143-3

Query Match 58.8%; Score 20; DB 2; Length 829;
Best Local Similarity 82.1%; Pred. No. 76;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 6 CTTTGCTACTGCTGCTGACCTGACCC 33
DB 62 CTTGGGGCTGCTGCTGACCTGCTGCC 35

RESULT 13

US-09-256-331-3/c
Sequence 3, Application US/09256331
Patent No. 611077
GENERAL INFORMATION:
APPLICANT: NAHUM SONENBERG
APPLICANT: ARNIM PAUSE
APPLICANT: JOE B. HARFORD
TITLE OF INVENTION: METHODS FOR TREATING
TITLE OF INVENTION: HORMONE DISORDERS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/256,331
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/294,143
FILING DATE: August 22, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 202/060
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 829 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-256-331-3

Query Match 58.8%; Score 20; DB 3; Length 829;
Best Local Similarity 82.1%; Pred. No. 76;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 6 CTTTGCTACTGCTGCTGACCTGACCC 33
DB 62 CTTGGGGCTGCTGCTGACCTGCTGCC 35

RESULT 14

US-09-593-483-3/c
Sequence 3, Application US/09593483
Patent No. 6410715
GENERAL INFORMATION:
APPLICANT: NAHUM SONENBERG
APPLICANT: ARNIM PAUSE
APPLICANT: JOE B. HARFORD
TITLE OF INVENTION: METHODS FOR TREATING
TITLE OF INVENTION: HORMONE DISORDERS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/593,483
FILING DATE: 14-Jun-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/294,143
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 202/060
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 829 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-593-483-3

Query Match 58.8%; Score 20; DB 4; Length 829;
Best Local Similarity 82.1%; Pred. No. 76;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 6 CTTTGCTACTGCTGCTGACCTGACCC 33
DB 62 CTTGGGGCTGCTGCTGACCTGCTGCC 35

RESULT 15

US-09-489-039A-5244/c
Sequence 5244, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 26, 2005, 13:15:32 ; Search time 241.022 Seconds
(without alignments)
810.549 Million cell updates/sec

Title: US-10-085-612A-2

Perfect score: 34

Sequence: 1 cgattcttctactgctgcagctgcagcccg 34

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	34	100.0	34	US-10-085-612-2	Sequence 2, Appl1
2	33	97.1	34	US-10-085-612-6	Sequence 6, Appl1
3	33	97.1	1254	US-10-085-612-4	Sequence 4, Appl1
4	22.8	67.1	1012	US-09-957-997-4	Sequence 4, Appl1
5	22.8	67.1	1345	US-09-943-115A-1	Sequence 1, Appl1
6	22.8	67.1	1345	US-10-146-575-3	Sequence 3, Appl1
7	22.8	67.1	1345	US-10-085-612-3	Sequence 3, Appl1
8	22.8	67.1	11186	US-09-957-997-1	Sequence 1, Appl1
9	22.8	67.1	13035	US-10-121-960C-14	Sequence 14, Appl1
10	22.8	67.1	15185	US-10-121-960C-17	Sequence 17, Appl1
11	21.6	63.5	481	US-10-027-632-72580	Sequence 72580, A
12	21.6	63.5	481	US-10-027-632-72580	Sequence 72580, A

C	13	21.4	62.9	599	13	US-10-027-632-285947	Sequence 285947,
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C	15	21.4	62.9	3800	16	US-10-240-425-355	Sequence 355, App
C	16	21.4	61.8	1442	16	US-10-424-599-64169	Sequence 64169, A
C	17	20.8	61.2	976	16	US-10-282-428-23816	Sequence 23816, A
C	18	20.6	60.6	30	15	US-10-215-432-41	Sequence 41, Appl1
C	19	20.2	60.0	394	16	US-10-424-599-31369	Sequence 31369, A
C	20	20.2	59.4	470	10	US-09-918-995-24594	Sequence 24594, A
C	21	20.2	59.4	672	13	US-10-027-632-253693	Sequence 253693,
C	22	20.2	59.4	672	13	US-10-027-632-253693	Sequence 253693,
C	23	20.2	59.4	923	16	US-10-425-114-34526	Sequence 34526, A
C	24	20.2	59.4	968	18	US-10-739-930-2556	Sequence 2556, App
C	25	20.2	59.4	994	10	US-09-934-455-489	Sequence 489, App
C	26	20.2	59.4	994	17	US-10-767-701-9995	Sequence 9995, App
C	27	20.2	59.4	1149	18	US-10-425-115-97578	Sequence 97578, A
C	28	20.2	59.4	4285	17	US-10-303-327-4	Sequence 4, Appl1
C	29	20.2	59.4	4308	10	US-09-394-1428-23	Sequence 23, Appl1
C	30	20.2	59.4	4308	17	US-10-782-627-23	Sequence 23, Appl1
C	31	20.2	59.4	5526	18	US-10-357-930-23191	Sequence 23191, A
C	32	20.2	59.4	5526	18	US-10-357-930-23191	Sequence 23191, A
C	33	20.2	59.4	35425	17	US-10-322-696-91	Sequence 29057, A
C	34	20.2	58.8	357	16	US-10-641-643-1445	Sequence 91, Appl1
C	35	20.2	58.8	551	18	US-10-723-860-549	Sequence 1445, App
C	36	20.2	58.8	627	9	US-09-770-149-726	Sequence 149, App
C	37	20.2	58.8	802	9	US-09-925-301-322	Sequence 726, App
C	38	20.2	58.8	831	15	US-10-353-929-57	Sequence 322, App
C	39	20.2	58.8	1358	10	US-09-877-843-11	Sequence 57, Appl1
C	40	20.2	58.8	1358	16	US-10-403-161-25	Sequence 25, Appl1
C	41	20.2	58.8	2059	16	US-10-276-774-864	Sequence 864, App
C	42	20.2	58.8	2173	16	US-10-425-114-21375	Sequence 21375, A
C	43	20.2	58.8	2758	18	US-10-425-115-3898	Sequence 3898, App
C	44	20.2	58.8	13358	18	US-10-719-993-6923	Sequence 6923, App
C	45	20.2	58.8	37443	18	US-10-719-993-6853	Sequence 6853, App

ALIGNMENTS

RESULT 1
US-10-085-612-2
; Sequence 2, Application US/10085612
; Publication No. US20030096251A1
; GENERAL INFORMATION:
; APPLICANT: Guida, Marco
; APPLICANT: Hall, Jeff
; APPLICANT: Petros, William
; APPLICANT: Vredenburg, James
; APPLICANT: Colvin, Oliver
; APPLICANT: Marks, Jeffrey
; TITLE OF INVENTION: Methods for Evaluating the Ability to Metabolize Pharmaceuticals
; FILE REFERENCE: 4389-5-C1
; CURRENT APPLICATION NUMBER: US/10/085,612
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/144,367
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/271,630
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 34
TYPE: DNA
ORGANISM: Homo sapiens
US-10-085-612-2
Query Match 100.0%; Score 34; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00063;
Matches 34; Conservative 0; Mismatches 0; Gaps 0;
DB 1 CGATTCTTCTACTGCTGCAGCTGCAGCCCG 34
1 CGATTCTTCTACTGCTGCAGCTGCAGCCCG 34

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RESULT 2
US-10-085-612-6
; Sequence 6, Application US/10085612
; Publication No. US20030096251A1
; GENERAL INFORMATION:
; APPLICANT: Guida, Marco
; APPLICANT: Hall, Jeff
; APPLICANT: Petros, William
; APPLICANT: Vredenburg, James
; APPLICANT: Colvin, Oliver
; APPLICANT: Marks, Jeffrey
; TITLE OF INVENTION: Methods for Evaluating the Ability to Metabolize Pharmaceuticals
; FILE REFERENCE: 4389-5-C1
; CURRENT APPLICATION NUMBER: US/10/085,612
; PRIOR FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/144,367
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/271,630
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-612-6

Query Match          97.1%; Score 33; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CGATCTTTGCTAGCTGCGTGCAGCCCC 33

RESULT 3
US-10-085-612-4
; Sequence 4, Application US/10085612
; Publication No. US20030096251A1
; GENERAL INFORMATION:
; APPLICANT: Guida, Marco
; APPLICANT: Hall, Jeff
; APPLICANT: Petros, William
; APPLICANT: Vredenburg, James
; APPLICANT: Colvin, Oliver
; APPLICANT: Marks, Jeffrey
; TITLE OF INVENTION: Methods for Evaluating the Ability to Metabolize Pharmaceuticals
; FILE REFERENCE: 4389-5-C1
; CURRENT APPLICATION NUMBER: US/10/085,612
; PRIOR FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/144,367
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/271,630
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 1254
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-612-4

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Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CGATCTTTGCTAGCTGCGTGCAGCCCC 33
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RESULT 4
US-09-957-997-4
; Sequence 4, Application US/09957997
; Patent No. US20020150915A1
; GENERAL INFORMATION:
; APPLICANT: Berkenstam, Anders
; APPLICANT: Bertilsson, Gran
; APPLICANT: Blomquist, Patrik
; TITLE OF INVENTION: PROMOTER SEQUENCES
; FILE REFERENCE: 13425-046001
; CURRENT APPLICATION NUMBER: US/09/957,997
; CURRENT FILING DATE: 2001-09-21
; EARLIER APPLICATION NUMBER: SE 0003393-6
; EARLIER FILING DATE: 2000-09-22
; EARLIER APPLICATION NUMBER: 60/238,895
; EARLIER FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1012
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-957-997-4

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Db 947 TGCTACTGCTGCTGAGCTGCAGCCCCG 972

RESULT 5
US-09-943-115A-1
; Sequence 1, Application US/09943115A
; Publication No. US20030017469A1
; GENERAL INFORMATION:
; APPLICANT: SEQUENOM, Inc.
; APPLICANT: Risinger, Carl
; APPLICANT: Andersson, Maria
; APPLICANT: Lewander, Tommy
; APPLICANT: Olaisson, Erik
; TITLE OF INVENTION: DETECTION OF CYP3A4 AND CYP2C9
; FILE REFERENCE: 52459-20021.00
; CURRENT APPLICATION NUMBER: US/09/943,115A
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: UK 0021286.0
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-943-115A-1

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Best Local Similarity 92.3%; Pred. No. 18;
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Db 1035 TGCTACTGCTGCTGAGCTGCAGCCCCG 1060

RESULT 6
US-10-146-575-3
; Sequence 3, Application US/10146575
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1 Publication No. US20030059800A1
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3 GENERAL INFORMATION:
4
5 APPLICANT: Lichteir, Jay
6
7 APPLICANT: Guido, Marco
8
9 TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
10
11 FILE REFERENCE: SEQ-12P
12
13 CURRENT APPLICATION NUMBER: US/10/146,575
14
15 CURRENT FILING DATE: 2002-05-14
16
17 PRIOR APPLICATION NUMBER: US/09/144,367
18
19 PRIOR FILING DATE: 1998-08-31
20
21 NUMBER OF SEQ ID NOS: 58
22
23 SOFTWARE: FaastSeq for Windows Version 3.0
24
25 SEQ ID NO 3
26
27 LENGTH: 1345
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29 TYPE: DNA
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31 ORGANISM: H. sapiens
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33 FEATURE:
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39 US-10-146-575-3

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Oy 9 TGCTACTGGCTGCAGCTGCAGCCCCG 34
 Db 1035 TGCTACTGGCTGCAGCTGCAGCCCCG 1060

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RESULT 7
US-10-085-612-3
; Sequence 3, Application US/10085612
; Publication No. US20030096251A1
; GENERAL INFORMATION:
; APPLICANT: Guida, Marco
; APPLICANT: Hall, Jeff
; APPLICANT: Petroe, William
; APPLICANT: Vredenburg, James
; APPLICANT: Colvin, Oliver
; APPLICANT: Marks, Jeffrey
; TITLE OF INVENTION: Methods for Evaluating the Ability to Metabolize Pharmaceuticals
; TITLE OF INVENTION: Compositions Therefor
; FILE REFERENCE: 4389-5-C1
; CURRENT APPLICATION NUMBER: US/10/085,612
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/144,367
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/271,630
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-085-612-3

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Db 1035 TGCTACTGGCTGCAGCTCCAGCCCTG 1060

RESULT 8
US-09-957-997-1
; Sequence 1, Application US/09957997
; Patent No. US20020150915A1
; GENERAL INFORMATION:
; APPLICANT: Berkenstram, Anders

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1  APPLICANT: Bertilsson, Grah
2  APPLICANT: Blomquist, Patrik
3  TITLE OF INVENTION: PROMOTER SEQUENCES
4  FILE REFERENCE: 13425-046001
5  CURRENT APPLICATION NUMBER: US/09/957, 997
6  CURRENT FILING DATE: 2001-09-21
7  EARLIER APPLICATION NUMBER: SE 0003393-6
8  EARLIER FILING DATE: 2000-09-22
9  EARLIER APPLICATION NUMBER: 60/228, 895
10 EARLIER FILING DATE: 2000-10-10
11 NUMBER OF SEQ ID NOS: 15
12 SOFTWARE: FastSeq for Windows Version 4.0
13 SEQ ID NO 1
14 LENGTH: 11186
15 TYPE: DNA
16 ORGANISM: Homo sapiens
17
18 US-09-957-997-1

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Query Match	67.1%	Score 22.8;	DB 9;	Length 1116;
Best Local Similarity	92.3%	Pred. No. 21;		
Matches	24;	Conservative	0;	Mismatches 2;
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			Gaps	0;

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RESULT 9
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; Sequence 14, Application US/10121960C
; Publication No. US20030145341A1
; GENERAL INFORMATION:
; APPLICANT: ZHANG, Weisheng
; APPLICANT: CONTAG, Pamela
; APPLICANT: PURCHIO, Anthony
; APPLICANT: HASHIMA, Sandy
; APPLICANT: MA, Shitley
; APPLICANT: NAMOTKA, Kevin
; TITLE OF INVENTION: ISOLATION AND IDENTIFICATION OF MOUSE AND HUMAN
; TITLE OF INVENTION: TRANSCRIPTOM CONTROL ELEMENTS ASSOCIATED WITH
; FILE REFERENCE: 9400-0014 / PXE-014.US
; CURRENT APPLICATION NUMBER: US/10/121,960C
; CURRENT FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 13035
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human CYP3A4 gene locus
US-10-121-960C-14

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Query Match	67.1%	Score 22.8;	DB 15;	Length 13035;
Best Local Similarity	92.3%	Pred. No. 21;		
Matches 24;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;

Oy 9 TGGTACTGGCTGCAGCTGCAGCCCCG 34
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 Db 12860 TGGTACTGGCTGCAGCTCCAGCCCTG 12885
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RESULT 10
US-10-121-960C-17
; Sequence 17, Application US/10121960C
; Publication No. US20030145341A1
; GENERAL INFORMATION:
; APPLICANT: ZHANG, Weisheng
; APPLICANT: CONTAG, Pamela
; APPLICANT: PURCHIO, Anthony
; APPLICANT: HASHIMA, Sandy
; APPLICANT: MA, Shitley

GenCore version 5.1.6
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Run on: January 26, 2005, 11:30:01 ; Search time 30.0667 Seconds
(without alignments)
520.089 Million cell updates/sec

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Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

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Post-processing: Minimum Match 0%
Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	22	100.0	1345	US-09-144-367-3	Sequence 3, Appl
4	18.8	85.5	5400	US-09-134-000C-1773	Sequence 1773, Ap
5	17.2	78.2	752	US-09-008-979A-8	Sequence 8, Appl
6	17.2	78.2	752	US-09-460-618-8	Sequence 8, Appl
7	17.2	78.2	752	US-09-310-235B-8	Sequence 8, Appl
8	16.2	73.6	211	US-09-513-999C-21256	Sequence 21256, A
9	16.2	73.6	428	US-09-621-976-15687	Sequence 15687, A
10	16.2	73.6	640	US-09-034-088A-26	Sequence 26, Appl
11	16.2	73.6	640	US-09-781-811-26	Sequence 26, Appl
12	16.2	73.6	692	US-08-465-283A-1	Sequence 1, Appl
13	16.2	73.6	692	US-08-463-387A-1	Sequence 1, Appl
14	16.2	73.6	692	US-09-102-977-1	Sequence 1, Appl
15	16.2	73.6	692	US-09-034-088A-1	Sequence 1, Appl
16	16.2	73.6	692	US-09-781-811-1	Sequence 1, Appl
17	15.8	71.8	96109	US-09-596-002-35	Sequence 35, Appl
18	15.8	71.8	99916	US-09-816-095-3	Sequence 3, Appl
19	15.6	70.9	343	US-09-621-976-654	Sequence 654, App
20	15.6	70.9	393	US-09-270-767-7434	Sequence 27434, A
21	15.6	70.9	441	US-09-248-796A-11615	Sequence 11615, A
22	15.6	70.9	834	US-09-543-681A-355	Sequence 355, App
23	15.6	70.9	975	US-09-543-681A-3164	Sequence 3164, App
24	15.6	70.9	1353	US-09-270-767-11795	Sequence 11795, A
25	15.6	70.9	1379	US-08-437-607A-1	Sequence 4, Appl
26	15.6	70.9	1380	US-08-437-607A-4	Sequence 4, Appl
27	15.6	70.9	2733	US-08-676-967-3	Sequence 3, Appl

C	28	15.6	70.9	2733	1	US-08-676-974-3	Sequence 3, Appl
C	29	15.6	70.9	2733	2	US-09-098-487-3	Sequence 3, Appl
C	30	15.6	70.9	75395	4	US-09-984-890-3	Sequence 3, Appl
C	31	15.6	70.9	75395	4	US-10-274-194-3	Sequence 3, Appl
C	32	15.4	70.0	11212	4	US-09-248-796A-2520	Sequence 2520, Ap
C	33	15.4	70.0	1650	4	US-09-579-288-3	Sequence 3, Appl
C	34	15.4	70.0	2403	4	US-09-907-794A-226	Sequence 226, App
C	35	15.4	70.0	2403	4	US-09-905-125A-226	Sequence 226, App
C	36	15.4	70.0	2403	4	US-09-902-775A-226	Sequence 226, App
C	37	15.4	70.0	2403	4	US-09-906-700-226	Sequence 226, App
C	38	15.4	70.0	2403	4	US-09-903-603A-226	Sequence 226, App
C	39	15.4	70.0	2534	4	US-09-579-288-1	Sequence 1, Appl
C	40	15.4	70.0	2534	4	US-09-579-288-4	Sequence 4, Appl
C	41	15.2	69.1	443	4	US-09-513-999C-31715	Sequence 31715, A
C	42	15.2	69.1	450	4	US-09-540-236-681	Sequence 681, App
C	43	15.2	69.1	488	4	US-09-621-976-2091	Sequence 2091, App
C	44	15.2	69.1	493	4	US-09-621-976-16615	Sequence 16615, A
C	45	15.2	69.1	544	4	US-09-513-999C-12485	Sequence 12485, A

ALIGNMENTS

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RESULT 1
US-09-372-339-1
Sequence 1, Application US/09372339
Patent No. 6174684
GENERAL INFORMATION:
APPLICANT: Redbeck, Timothy
APPLICANT: Felix, Carolyn
TITLE OF INVENTION: CYP3A4 NFSE Variant and Methods of Use Therefor
FILE REFERENCE: PENN-0695
CURRENT APPLICATION NUMBER: US/09/372.339
EARLIER FILING DATE: 1999-08-11
EARLIER APPLICATION NUMBER: 60/096,586
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 1345
ORGANISM: Homo sapiens
US-09-372-339-1

Query Match      100.0%; Score 22; DB 3; Length 1345;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 ATCTGTAGTGCTGCTTGTGG 22
Db      745 ATCTGTAGTGCTGCTTGTGG 766

RESULT 2
US-09-372-339-2
Sequence 2, Application US/09372339
Patent No. 6174684
GENERAL INFORMATION:
APPLICANT: Redbeck, Timothy
APPLICANT: Felix, Carolyn
TITLE OF INVENTION: CYP3A4 NFSE Variant and Methods of Use Therefor
FILE REFERENCE: PENN-0695
CURRENT APPLICATION NUMBER: US/09/372.339
EARLIER FILING DATE: 1999-08-11
EARLIER APPLICATION NUMBER: 60/096,586
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 1345
ORGANISM: Homo sapiens
US-09-372-339-2
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Query Match 100.0%; Score 22; DB 3; Length 1345;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCTGTAGTGTGCTTGTGG 22
|||||
Db 745 ATCTGTAGTGTGCTTGTGG 766

RESULT 3
US-09-144-367-3
; Sequence 3, Application US/09144367
; Patent No. 6432639
; GENERAL INFORMATION:
; APPLICANT: Lichter, Jay
; APPLICANT: Guido, Marco
; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
; FILE REFERENCE: SEQ-12P
; CURRENT APPLICATION NUMBER: US/09/144,367
; CURRENT FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/058,612
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: Other
; LOCATION: (0)...(0)
US-09-144-367-3

Query Match 100.0%; Score 22; DB 4; Length 1345;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCTGTAGTGTGCTTGTGG 22
|||||
Db 745 ATCTGTAGTGTGCTTGTGG 766

RESULT 4
US-09-134-000C-1773/c
; Sequence 1773, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1773
; LENGTH: 5400
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (30)...(30)
; OTHER INFORMATION: Nucleotide 30 is "n" wherein "n" = any nucleotide.
US-09-134-000C-1773

Query Match 85.5%; Score 18.8; DB 4; Length 5400;
Best Local Similarity 90.9%; Pred. No. 7.4;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATCTGTAGTGTGCTTGTGG 22

Db 3834 ATCTGAAGTGTGCTTGTGG 3813

RESULT 5
US-09-008-979A-8
; Sequence 8, Application US/0908979A
; Patent No. 6080914
; GENERAL INFORMATION:
; APPLICANT: Conner, Timothy W.
; TITLE OF INVENTION: Strawberry Promoters and Genes
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carmen Rodriguez, Paralegal, Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/008,979A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Kammerer, Patricia A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: MOBT:058 (38-21(10613)A)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 787-1438
; TELEFAX: (713) 789-2679
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-09-008-979A-8

Query Match 78.2%; Score 17.2; DB 3; Length 752;
Best Local Similarity 86.4%; Pred. No. 31;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATCTGTAGTGTGCTTGTGG 22
|||||
Db 305 ATCTGTAGTGTGCTTGTGG 326

RESULT 6
US-09-460-618-8
; Sequence 8, Application US/09460618
; Patent No. 6235482
; GENERAL INFORMATION:
; APPLICANT: Conner, Timothy W.
; TITLE OF INVENTION: Strawberry Promoters and Genes
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carmen Rodriguez, Paralegal, Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/460,618
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/008,979
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kammerer, Patricia A.
REGISTRATION NUMBER: 29,775
TELECOMMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER: MOBT-058 (38-21(10613)A)
TELEPHONE: (713) 787-1438
TELEFAX: (713) 789-2679
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 752 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-09-460-618-8

Query Match 78.2%; Score 17.2; DB 3; Length 752;
Best Local Similarity 86.4%; Pred. No. 31;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATCTGTAGTGTGGCTTGTGG 22
DB 305 ATCTGTAGTGTGACCTTGTGG 326

RESULT 7
US-09-310-2358-8
Sequence 8, Application US/093102358
Patent No. 6392030
GENERAL INFORMATION:
APPLICANT: Comer, Timothy
TITLE OF INVENTION: STRAMBERY PROMOTERS AND GENES
FILE REFERENCE: MOBT058-1 (11899,0058, DVUS00)
CURRENT APPLICATION NUMBER: US/09/310,2358
CURRENT FILING DATE: 1998-05-12
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.0
SEQ ID NO 8
LENGTH: 752
TYPE: DNA
ORGANISM: fragaria x ananassa
US-09-310-2358-8

Query Match 78.2%; Score 17.2; DB 3; Length 752;
Best Local Similarity 86.4%; Pred. No. 31;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATCTGTAGTGTGGCTTGTGG 22
DB 305 ATCTGTAGTGTGACCTTGTGG 326

RESULT 8
US-09-513-999C-21256/c
Sequence 21256, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59, US2, RBG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681

SOFTWARE: Patent.pm
SEQ ID NO 21256
LENGTH: 211,
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 13
OTHER INFORMATION: r=a or g
US-09-513-999C-21256

Query Match 73.6%; Score 16.2; DB 4; Length 211;
Best Local Similarity 85.7%; Pred. No. 76;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATCTGTAGTGTGGCTTGTGG 21
DB 195 ATCTGTAGTGTGGCTTGTGG 175

RESULT 9
US-09-621-976-15687
Sequence 15687, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET, 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 15687
LENGTH: 428
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-15687

Query Match 73.6%; Score 16.2; DB 4; Length 428;
Best Local Similarity 85.7%; Pred. No. 86;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATCTGTAGTGTGGCTTGTGG 21
DB 329 ATCTGTAGTGTGGCTTGTGG 349

RESULT 10
US-09-034-088A-26
Sequence 26, Application US/09034088A
Patent No. 6310034
GENERAL INFORMATION:
APPLICANT: WOYCHIK, RICHARD P.
APPLICANT: BULTMAN, SCOTT J.
APPLICANT: MITCHARD, EDWARD J.
TITLE OF INVENTION: METHODS AND POLYPEPTIDES ENCODED BY AGOUTI GENE
FILE REFERENCE: 4310,001600
CURRENT APPLICATION NUMBER: US/09/034,088A
CURRENT FILING DATE: 1998-03-03
PRIOR APPLICATION NUMBER: 08/064,385
PRIOR FILING DATE: 1993-05-21
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 26
LENGTH: 640
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-034-088A-26

Query Match 73.6%; Score 16.2; DB 3; Length 640;
Best Local Similarity 85.7%; Pred. No. 92;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TCTGTAGTGTGGCTTGTGG 22
Db 515 TCTGTGGTGGGCTTGTGG 535

RESULT 11

US-09-781-811-26
Sequence 26, Application US/09781811
Patent No. 6514747
GENERAL INFORMATION:
APPLICANT: WOYCHIK, RICHARD P.
APPLICANT: BULTMAN, SCOTT J.
APPLICANT: MICHAUD, EDWARD J.
TITLE OF INVENTION: AGOUTI POLYNUCLEOTIDE COMPOSITIONS AND METHODS OF USE
FILE REFERENCE: 4310.001682
CURRENT FILING DATE: 2001-02-12
PRIOR APPLICATION NUMBER: 09/034,088
PRIOR FILING DATE: 1998-03-03
PRIOR APPLICATION NUMBER: 08/064,385
PRIOR FILING DATE: 1993-05-21
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 26
LENGTH: 640
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-781-811-26

Query Match 73.6%; Score 16.2; DB 4; Length 640;
Best Local Similarity 85.7%; Pred. No. 92;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TCTGTAGTGTGGCTTGTGG 22
Db 515 TCTGTGGTGGGCTTGTGG 535

RESULT 12

US-08-465-293A-1
Sequence 1, Application US/08465293A
Patent No. 5789651
GENERAL INFORMATION:
APPLICANT: WOYCHIK, RICHARD P.
TITLE OF INVENTION: Isolation and Characterization of
TITLE OF INVENTION: Agouti A Diabetes/Obesity Related Gene.
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan
STREET: 555 13th Street, N.W., Suite #480 West
CITY: Washington
STATE: District of Columbia
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,293A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/064,385
FILING DATE: 21-MAY-1993

ATTORNEY/AGENT INFORMATION:
NAME: Edward A. Pennington
REGISTRATION NUMBER: 32,588
REFERENCE/DOCKET NUMBER: 2240-7054
TELEPHONE: (202) 857-7887
TELEFAX: (202) 857-7929
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 692 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:

ORGANISM: Mouse
STRAIN: C3H Strain
DEVELOPMENTAL STAGE: Neonatal or Adult
TISSUE TYPE: Neonatal skin or adult Ay 1a1sgo kidney or
TISSUE TYPE: testis.
IMMEDIATE SOURCE:

LIBRARY: Neonatal skin cDNA
POSITION IN GENOME:
CHROMOSOME/SEGMENT: Agouti locus of mouse chromosome 2.
FEATURE:

NAME/KEY: Agouti locus
IDENTIFICATION METHOD: Experimental
OTHER INFORMATION: In addition to hair color in mice, the
OTHER INFORMATION: Agouti gene is responsible for embryonic lethality, obesity,
OTHER INFORMATION: diabetes, and the development of tumor in a wide variety of
OTHER INFORMATION: tissues.

PUBLICATION INFORMATION:
AUTHORS: Scott J. Boltman, Edward J. Michaud, and Richard
TITLE: Molecular Characterization of the Mouse Agouti
TITLE: Locus
JOURNAL: Submitted to CELL
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 692
US-08-465-293A-1

Query Match 73.6%; Score 16.2; DB 1; Length 692;
Best Local Similarity 85.7%; Pred. No. 94;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TCTGTAGTGTGGCTTGTGG 22
Db 567 TCTGTGGTGGGCTTGTGG 587

RESULT 13

US-08-463-387A-1
Sequence 1, Application US/08463387A
Patent No. 5843652
GENERAL INFORMATION:
APPLICANT: WOYCHIK, RICHARD P.
TITLE OF INVENTION: Isolation and Characterization of
TITLE OF INVENTION: Agouti A Diabetes/Obesity Related Gene.
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan
STREET: 555 13th Street, N.W., Suite #480 West
CITY: Washington
STATE: District of Columbia
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,387A

FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/064,385
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Edward A. Pennington
REGISTRATION NUMBER: 32,588
REFERENCE/DOCKET NUMBER: 2240-7054
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 857-7887
TELEFAX: (202) 857-7929
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 692 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Mouse
STRAIN: C3H strain
DEVELOPMENTAL STAGE: Neonatal or Adult
TISSUE TYPE: Neonatal skin or adult Ay isleiso kidney or
TISSUE TYPE: testis.
IMMEDIATE SOURCE:
LIBRARY: Neonatal skin cDNA
POSITION IN GENOME:
CHROMOSOME/SEGMENT: Agouti locus of mouse chromosome 2.
FEATURE:
NAME/KEY: Agouti locus
IDENTIFICATION METHOD: Experimental
OTHER INFORMATION: In addition to hair color in mice, the
OTHER INFORMATION: Agouti gene is responsible for embryonic lethality, obesity,
OTHER INFORMATION: diabetes, and the development of tumor in a wide variety of
OTHER INFORMATION: tissues.
PUBLICATION INFORMATION:
AUTHORS: Scott J. Boltman, Edward J. Micaud, and Richard
AUTHORS: P. Moychik
TITLE: Molecular Characterization of the Mouse Agouti
TITLE: Locus
JOURNAL: Submitted to CELL
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 692
US-08-463-387A-1
Query Match 73.6%; Score 16.2; DB 2; Length 692;
Best Local Similarity 85.7%; Pred. No. 94;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 2 TCTGTAGTGTGGCTTGTGG 22
DB 567 TCTGTGGTGGGCTTGTGG 587
RESULT 14
US-09-102-977-1
Sequence 1, Application US/09102977
Patent No. 6080550
GENERAL INFORMATION:
APPLICANT: Moychik, Richard P.
TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF AGOUTI
TITLE OF INVENTION: A DIABETES/OBESITY RELATED GENE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/102,977
FILING DATE: 22-JUN-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/899,134
FILING DATE: 23-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/462,732
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: ORNL:014--1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512)418-3000
TELEFAX: (512)474-7577
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 692 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 83..475
US-09-102-977-1

Query Match 73.6%; Score 16.2; DB 3; Length 692;
Best Local Similarity 85.7%; Pred. No. 94;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 2 TCTGTAGTGTGGCTTGTGG 22
DB 567 TCTGTGGTGGGCTTGTGG 587

RESULT 15
US-09-034-088A-1
Sequence 1, Application US/09034088A
Patent No. 6310034
GENERAL INFORMATION:
APPLICANT: MOYCHIK, RICHARD P.
APPLICANT: BULTMAN, SCOTT J.
APPLICANT: MICHAUD, EDWARD J.
TITLE OF INVENTION: METHODS AND POLYPEPTIDES ENCODED BY AGOUTI GENE
FILE REFERENCE: 4310.001600
CURRENT APPLICATION NUMBER: US/09/034,088A
CURRENT FILING DATE: 1998-03-03
PRIOR APPLICATION NUMBER: 08/064,385
PRIOR FILING DATE: 1993-05-21
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 692
TYPE: DNA
ORGANISM: Mus musculus
US-09-034-088A-1

Query Match 73.6%; Score 16.2; DB 3; Length 692;
Best Local Similarity 85.7%; Pred. No. 94;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 2 TCTGTAGTGTGGCTTGTGG 22
DB 567 TCTGTGGTGGGCTTGTGG 587

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 26, 2005, 13:15:32 ; Search time 155.956 Seconds
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Title: US-10-085-612A-17

Perfect score: 22

Sequence: 1 atctgtacgtgtgctgtctgtcg 22

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Gapop 10.0 , Gapext 1.0

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Maximum Match 100%

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- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	1345	10	US-09-943-115A-1
2	22	100.0	1345	14	US-10-146-575-3
3	22	100.0	1345	14	US-10-085-612-3
4	22	100.0	13035	15	US-10-121-960C-14
5	22	100.0	15185	15	US-10-121-960C-17
6	20	90.9	26	18	US-10-114-908-9
7	19.4	88.2	33488	15	US-10-085-117-235
8	18.8	85.5	1012	9	US-09-957-997-4
9	18.8	85.5	7053	9	US-09-070-927A-78
10	18.8	85.5	11186	9	US-09-957-997-1
11	17.8	80.9	1378	9	US-09-820-893-28
12	17.8	80.9	1378	16	US-10-607-565-28

13	17.2	78.2	615	18	US-10-425-115-172581	Sequence 172581,
14	17.2	78.2	1254	14	US-10-085-612-4	Sequence 4, Appl1
15	17.2	78.2	4170	17	US-10-602-441-5	Sequence 5, Appl1
16	17.2	78.2	8943	16	US-10-257-166-47	Sequence 47, Appl1
17	17.2	78.2	130427	14	US-10-175-523-87	Sequence 87, Appl1
18	16.8	76.4	417	17	US-10-437-963-94546	Sequence 94546, A
19	16.8	76.4	606	13	US-10-027-632-69617	Sequence 69617, A
20	16.8	76.4	606	13	US-10-027-632-294476	Sequence 294476, A
21	16.8	76.4	606	13	US-10-027-632-294477	Sequence 294477, A
22	16.8	76.4	606	13	US-10-027-632-294477	Sequence 294477, A
23	16.8	76.4	606	15	US-10-027-632-69617	Sequence 69617, A
24	16.8	76.4	606	15	US-10-027-632-69618	Sequence 69618, A
25	16.8	76.4	606	15	US-10-027-632-294476	Sequence 294476, A
26	16.8	76.4	606	15	US-10-027-632-294477	Sequence 294477, A
27	16.8	76.4	632	18	US-10-425-115-51727	Sequence 51727, A
28	16.8	76.4	707	13	US-10-027-632-243832	Sequence 243832,
29	16.8	76.4	707	13	US-10-027-632-243833	Sequence 243833,
30	16.8	76.4	707	13	US-10-027-632-243834	Sequence 243834,
31	16.8	76.4	707	15	US-10-027-632-243832	Sequence 243832,
32	16.8	76.4	707	15	US-10-027-632-243833	Sequence 243833,
33	16.8	76.4	707	15	US-10-027-632-243834	Sequence 243834,
34	16.8	76.4	729	13	US-10-027-632-26514	Sequence 26514, A
35	16.8	76.4	729	13	US-10-027-632-26515	Sequence 26515, A
36	16.8	76.4	729	15	US-10-027-632-26514	Sequence 26514, A
37	16.8	76.4	729	15	US-10-027-632-26515	Sequence 26515, A
38	16.8	76.4	2167	15	US-10-106-698-1532	Sequence 1532, Ap
39	16.8	76.4	2502	16	US-10-424-599-130260	Sequence 130260,
40	16.8	76.4	3242	16	US-10-108-260A-1314	Sequence 1314, Ap
41	16.8	76.4	31834	9	US-09-764-847-1612	Sequence 1612, Ap
42	16.8	76.4	31834	14	US-10-092-154-1612	Sequence 1612, Ap
43	16.8	76.4	32035	9	US-09-764-847-1611	Sequence 1611, Ap
44	16.8	76.4	32035	14	US-10-092-154-1611	Sequence 1611, Ap
45	16.4	74.5	568	17	US-10-437-963-16133	Sequence 16133, A

ALIGNMENTS

RESULT 1
US-09-943-115A-1
; Sequence 1, Application US/09943115A
; Publication No. US20030017469A1
; GENERAL INFORMATION:
; APPLICANT: SEQUENOM, Inc.
; APPLICANT: Risinger, Carl
; APPLICANT: Andersson, Maria
; APPLICANT: Lewander, Tommy
; APPLICANT: Olafsson, Erik
; TITLE OF INVENTION: DETECTION OF CYP3A4 AND CYP2C9
; TITLE OF INVENTION: POLYMORPHISMS
; FILE REFERENCE: 52459-20021.00
; CURRENT APPLICATION NUMBER: US/09/943, 115A
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: UK 0021286.0
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-943-115A-1
Query Match 100.0%; Score 22; DB 10; Length 1345;
Best local Similarity 100.0%; Pred. No. 2, 6;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cyt 1 ATCTGTAGTGTGCTGTGTGG 22
Db 745 ATCTGTAGTGTGCTGTGTGG 766
RESULT 2

US-10-146-575-3
; Sequence 3, Application US/10146575
; Publication No. US20030059800A1
; GENERAL INFORMATION:
; APPLICANT: Lichter, Jay
; APPLICANT: Guido, Marco
; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
; FILE REFERENCE: SEQ-12P
; CURRENT APPLICATION NUMBER: US/10/146,575
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US/09/144,367
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: Other
; LOCATION: (0)...(0)
US-10-146-575-3

Query Match 100.0%; Score 22; DB 14; Length 1345;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATCTGTAGTGTGGCTTGTGG 22
|||||
Db 745 ATCTGTAGTGTGGCTTGTGG 766

RESULT 3
US-10-085-612-3
; Sequence 3, Application US/10085612
; Publication No. US20030096251A1
; GENERAL INFORMATION:
; APPLICANT: Guida, Marco
; APPLICANT: Hall, Jeff
; APPLICANT: Petros, William
; APPLICANT: Vredenburg, James
; APPLICANT: Colvin, Oliver
; APPLICANT: Marks, Jeffrey
; TITLE OF INVENTION: Methods for Evaluating the Ability to Metabolize Pharmaceuticals
; FILE REFERENCE: 4389-5-C1
; CURRENT APPLICATION NUMBER: US/10/085,612
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/144,367
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/271,630
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-612-3

Query Match 100.0%; Score 22; DB 14; Length 1345;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATCTGTAGTGTGGCTTGTGG 22
|||||
Db 745 ATCTGTAGTGTGGCTTGTGG 766

RESULT 4
US-10-121-960C-14
; Sequence 14, Application US/10121960C
; Publication No. US20030145341A1

; GENERAL INFORMATION:
; APPLICANT: ZHANG, Weisheng
; APPLICANT: CONTAG, Pamela
; APPLICANT: PURCHIO, Anthony
; APPLICANT: HASHIMA, Sandy
; APPLICANT: MA, Shitley
; TITLE OF INVENTION: ISOLATION AND IDENTIFICATION OF MOUSE AND HUMAN
; TITLE OF INVENTION: TRANSCRIPTION CONTROL ELEMENTS ASSOCIATED WITH
; FILE REFERENCE: 9400-0014 / PXE-014.US
; CURRENT APPLICATION NUMBER: US/10/121,960C
; CURRENT FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 13035
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human CYP3A4 gene locus
US-10-121-960C-14

Query Match 100.0%; Score 22; DB 15; Length 13035;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATCTGTAGTGTGGCTTGTGG 22
|||||
Db 12570 ATCTGTAGTGTGGCTTGTGG 12591

RESULT 5
US-10-121-960C-17
; Sequence 17, Application US/10121960C
; Publication No. US20030145341A1
; GENERAL INFORMATION:
; APPLICANT: ZHANG, Weisheng
; APPLICANT: CONTAG, Pamela
; APPLICANT: PURCHIO, Anthony
; APPLICANT: HASHIMA, Sandy
; APPLICANT: MA, Shitley
; APPLICANT: NAMOTKA, Kevin
; TITLE OF INVENTION: ISOLATION AND IDENTIFICATION OF MOUSE AND HUMAN
; TITLE OF INVENTION: TRANSCRIPTION CONTROL ELEMENTS ASSOCIATED WITH
; FILE REFERENCE: 9400-0014 / PXE-014.US
; CURRENT APPLICATION NUMBER: US/10/121,960C
; CURRENT FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 15185
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CYP3A4-luc transgene
US-10-121-960C-17

Query Match 100.0%; Score 22; DB 15; Length 15185;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATCTGTAGTGTGGCTTGTGG 22
|||||
Db 12570 ATCTGTAGTGTGGCTTGTGG 12591

RESULT 6
US-10-114-908-9
; Sequence 9, Application US/10114908
; Publication No. US20040228222A1
; GENERAL INFORMATION:


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; APPLICANT: Luehreen, Kenneth R.
; TITLE OF INVENTION: P450 Single Nucleotide Polymorphism Biochip Analysis
; FILE REFERENCE: A-70398-1/RMS/DIR
; CURRENT APPLICATION NUMBER: US/10/114,908
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US 60/280,583
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 277
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-114-908-9

Query Match      90.9%; Score 20; DB 18; Length 26;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 CTGAGGTGGCTTGTGG 22
Db      1 CTGAGGTGGCTTGTGG 20

RESULT 7
US-10-085-117-235
; Sequence 235, Application US/10085117
; Publication No. US2003023334A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: 529452000121
; CURRENT APPLICATION NUMBER: US/10/085,117
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 235
; LENGTH: 33488
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: variation
; LOCATION: (1)..(33488)
; OTHER INFORMATION: n = any nucleotide
; US-10-085-117-235

Query Match      88.2%; Score 19.4; DB 15; Length 33488;
Best Local Similarity 95.2%; Pred. No. 44;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 ATCTGAGTGTGGCTTGTG 21
Db      1609 ATCTGATGTGTGGCTTGTG 1629

RESULT 8
US-09-957-997-4
; Sequence 4, Application US/09957997
; Patent No. US20020150915A1
; GENERAL INFORMATION:
; APPLICANT: Berkenstam, Anders
; APPLICANT: Bertilsson, Gran
; APPLICANT: Blomquist, Patrik
; TITLE OF INVENTION: PROMOTER SEQUENCES
; FILE REFERENCE: 13425-046001
; CURRENT APPLICATION NUMBER: US/09/957,997
; CURRENT FILING DATE: 2001-09-21
; EARLIER APPLICATION NUMBER: SE 0003393-6
; EARLIER FILING DATE: 2000-09-22
; EARLIER APPLICATION NUMBER: 60/238,895
```

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; EARLIER FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1012
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-957-997-4

Query Match      85.5%; Score 18.8; DB 9; Length 1012;
Best Local Similarity 90.9%; Pred. No. 74;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 ATCTGAGTGTGGCTTGTG 22
Db      668 ATCTGAGCATGGCTTGTG 689

RESULT 9
US-09-070-927A-78
; Sequence 78, Application US/09070927A
; Patent No. US20020120116A1
; GENERAL INFORMATION:
; APPLICANT: Charles A. Kunsch
; APPLICANT: Patrick J. Dillon
; APPLICANT: Steven Barash
; TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 982
; CORRESPONDENCE ADDRESS:
; ADDRESS: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,927A
; FILING DATE: 04-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/046,655
; FILING DATE: 1997-05-16
; APPLICATION NUMBER: 60/044,031
; FILING DATE: 1997-05-06
; APPLICATION NUMBER: 60/066,009
; FILING DATE: 1997-11-14
; ATTORNEY/AGENT INFORMATION:
; NAME: Kenley K. Hoover
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PB369
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7053 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 78:
; US-09-070-927A-78

Query Match      85.5%; Score 18.8; DB 9; Length 7053;
Best Local Similarity 90.9%; Pred. No. 79;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 ATCTGAGTGTGGCTTGTG 22
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Db 835 ATCTGAAGTGTGCTTGTGG 856

RESULT 10

US-09-957-997-1

; Sequence 1, Application US/09957997
; Patent No. US20020150915A1

; GENERAL INFORMATION:

; APPLICANT: Berkenstam, Anders

; APPLICANT: Bertleson, Gran

; APPLICANT: Blomquist, Patrik

; TITLE OF INVENTION: PROMOTER SEQUENCES

; FILE REFERENCE: 13425-046001

; CURRENT APPLICATION NUMBER: US/09/957,997

; CURRENT FILING DATE: 2001-09-21

; EARLIER APPLICATION NUMBER: SE 0003393-6

; EARLIER FILING DATE: 2000-09-22

; EARLIER APPLICATION NUMBER: 60/238,895

; EARLIER FILING DATE: 2000-10-10

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 11186

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-957-997-1

Query Match 85.5%; Score 18.8; DB 9; Length 11186;

Best Local Similarity 90.9%; Pred. No. 80;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATCTGAGTGTGCTTGTGG 22

Db 10785 ATCTGAGTGTGCTTGTGG 10806

RESULT 11

US-09-820-893-28

; Sequence 28, Application US/09820893

; Patent No. US20020076705A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 31 Human Secreted Proteins

; FILE REFERENCE: P2033P1

; CURRENT APPLICATION NUMBER: US/09/820,893

; CURRENT FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: 09/531,119

; PRIOR FILING DATE: 2000-03-20

; PRIOR APPLICATION NUMBER: 60/102,895

; PRIOR FILING DATE: 1998-10-02

; NUMBER OF SEQ ID NOS: 140

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 28

; LENGTH: 1378

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-820-893-28

Query Match 80.9%; Score 17.8; DB 9; Length 1378;

Best Local Similarity 90.5%; Pred. No. 2.1e+02;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TCTGTAGTGTGCTTGTGG 22

Db 417 TCTGTAGTGTGCTTGTGG 437

RESULT 12

US-10-607-565-28

; Sequence 28, Application US/10607565

; Publication No. US20040048294A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 31 Human Secreted Proteins

; FILE REFERENCE: P2033P1

; CURRENT APPLICATION NUMBER: US/10/607,565

; CURRENT FILING DATE: 2003-06-27

; PRIOR APPLICATION NUMBER: US/09/531,119

; PRIOR FILING DATE: 2000-03-20

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/101,546

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-23

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/102,895

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-02

; NUMBER OF SEQ ID NOS: 140

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 28

; LENGTH: 1378

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-607-565-28

Query Match 80.9%; Score 17.8; DB 16; Length 1378;

Best Local Similarity 90.5%; Pred. No. 2.1e+02;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TCTGTAGTGTGCTTGTGG 22

Db 417 TCTGTAGTGTGCTTGTGG 437

RESULT 13

US-10-425-115-172581

; Sequence 172581, Application US/10425115

; Publication No. US20040214272A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53222)B

; CURRENT APPLICATION NUMBER: US/10/425,115

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326

; SEQ ID NO 172581

; LENGTH: 615

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: MRT4577_88977C.1

US-10-425-115-172581

Query Match 78.2%; Score 17.2; DB 18; Length 615;

Best Local Similarity 86.4%; Pred. No. 3.9e+02;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATCTGAGTGTGCTTGTGG 22

Db 527 AGCTGAGTGTGCTTGTGG 548

RESULT 14

US-10-085-612-4

; Sequence 4, Application US/10085612

; Publication No. US20030096251A1

; GENERAL INFORMATION:

; APPLICANT: Guida, Marco

; APPLICANT: Hall, Jeff

; APPLICANT: Petros, William

; APPLICANT: Vredenburg, James

; APPLICANT: Colvin, Oliver

; APPLICANT: Marks, Jeffrey

; TITLE OF INVENTION: Methods for Evaluating the Ability to Metabolize Pharmaceuticals

; FILE REFERENCE: 4389-5-C1

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ORGANISM: *Homo sapiens*

Query Match 100.0%; Score 24; DB 3; Length 1345;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATCAGAACTCAAGTGAGCCAT 24
Db 870 TATCAGAACTCAAGTGAGCCAT 847

RESULT 3

US-09-144-367-3/C
; Sequence 3, Application US/09144367
; Patent No. 6432639
; GENERAL INFORMATION:
; APPLICANT: Guido, Jay
; APPLICANT: Guido, Marco
; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
; FILE REFERENCE: SEQ-12P
; CURRENT APPLICATION NUMBER: US/09/144,367
; CURRENT FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/058,612
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: Other
; LOCATION: (0) ... (0)
US-09-144-367-3

Query Match 100.0%; Score 24; DB 4; Length 1345;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATCAGAACTCAAGTGAGCCAT 24
Db 870 TATCAGAACTCAAGTGAGCCAT 847

RESULT 4

US-09-248-796A-2251
; Sequence 2251, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 2251
; LENGTH: 588
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-2251

Query Match 70.0%; Score 16.8; DB 4; Length 588;
Best Local Similarity 90.0%; Pred. No. 42;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ATCAGAACTCAAGTGAGC 21
Db 172 ATCAGAACTCAATTGATC 191

RESULT 5
US-08-222-719-6
; Sequence 6, Application US/08222719
; Patent No. 5846711
; GENERAL INFORMATION:
; APPLICANT: David D. Moore
; APPLICANT: Jae Moon Lee
; TITLE OF INVENTION: NUCLEAR HORMONE RECEPTOR-
; TITLE OF INVENTION: INTERACTING POLYPEPTIDES AND
; TITLE OF INVENTION: RELATED MOLECULES AND METHODS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,719
; FILING DATE: 04-April-1994
; CLASSIFICATION: 436
; APPLICATION NUMBER: 07/959,136
; FILING DATE: 30-October-1992
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/229001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 495
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-222-719-6

Query Match 69.2%; Score 16.6; DB 2; Length 495;
Best Local Similarity 82.6%; Pred. No. 52;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ATCAGAACTCAAGTGAGCCAT 24
Db 379 ATCAGAAATTAAGTCAGCCAT 401

RESULT 6

US-08-470-925-6
; Sequence 6, Application US/08470925
; Patent No. 586686
; GENERAL INFORMATION:
; APPLICANT: David D. Moore
; APPLICANT: Jae Moon Lee
; TITLE OF INVENTION: NUCLEAR HORMONE RECEPTOR-
; TITLE OF INVENTION: INTERACTING POLYPEPTIDES AND
; TITLE OF INVENTION: RELATED MOLECULES AND METHODS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts

COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,925
FILING DATE: 06-June-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/222,719
FILING DATE: 04-April-1994
CLASSIFICATION: 435
APPLICATION NUMBER: 07/969,136
FILING DATE: October 30, 1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/229003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 495
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-470-925-6

Query Match 69.2%; Score 16.6; DB 2; Length 495;
Best Local Similarity 82.6%; Pred. No. 52;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ATCAGAACTCAAGTGAGCCAT 24
DB 379 ATCAGAAATTAACTGAGCCAT 401

RESULT 7
US-08-471-613-6
Sequence 6, Application US/08471613
Patent No. 5962256
GENERAL INFORMATION:
APPLICANT: David D. Moore
APPLICANT: Jae Moon Lee
TITLE OF INVENTION: NUCLEAR HORMONE RECEPTOR-
INTERACTING POLYPEPTIDES AND
TITLE OF INVENTION: RELATED MOLECULES AND METHODS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,613
FILING DATE: 06-June-1995
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/222,719
FILING DATE: 04-April-1994

CLASSIFICATION: 436
APPLICATION NUMBER: 07/969,136
FILING DATE: October 30, 1992
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/229001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 495
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-471-613-6

Query Match 69.2%; Score 16.6; DB 2; Length 495;
Best Local Similarity 82.6%; Pred. No. 52;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ATCAGAACTCAAGTGAGCCAT 24
DB 379 ATCAGAAATTAACTGAGCCAT 401

RESULT 8
PCT-US93-10443-6
Sequence 6, Application PC/TUS9310443
GENERAL INFORMATION:
APPLICANT: David D. Moore
APPLICANT: Jae W. Lee
TITLE OF INVENTION: NUCLEAR HORMONE RECEPTOR-
INTERACTING POLYPEPTIDES AND
TITLE OF INVENTION: RELATED MOLECULES AND METHODS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10443
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,136
FILING DATE: October 30, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/099002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 495
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
PCT-US93-10443-6

Query Match 69.2%; Score 16.6; DB 5; Length 495;
Best Local Similarity 82.6%; Pred. No. 52;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ATCAGAACTCAAGTGCAGCCAT 24
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Db 379 ATCAGAAATTAAGTGCAGCAT 401

RESULT 9

US-09-102-528-28/c
; Sequence 28, Application US/09102528
; Patent No. 6207883
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: DNA Sequences
; NUMBER OF SEQUENCES: 32
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (ERO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/102,528
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB96/03191
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7815 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-102-528-28

Query Match 69.2%; Score 16.6; DB 3; Length 7815;
Best Local Similarity 82.6%; Pred. No. 95;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ATCAGAACTCAAGTGCAGCCAT 24
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Db 3868 ATCAGCACTGAAGTGCAGCCAT 3846

RESULT 10

US-09-621-976-13491/c
; Sequence 13491, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 13491
; LENGTH: 482
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-13491

Query Match 67.5%; Score 16.2; DB 4; Length 482;
Best Local Similarity 85.7%; Pred. No. 81;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 TCAGAACTCAAGTGCAGCCA 23
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Db 276 TCAGAGACTCAAGTGCAGCCA 256

RESULT 11

US-09-150-867-2
; Sequence 2, Application US/09150867
; Patent No. 6645748
; GENERAL INFORMATION:
; APPLICANT: Wood, Kenneth W.
; APPLICANT: Sakowicz, Roman
; APPLICANT: Goldstein, Lawrence S.B.
; APPLICANT: Cleveland, Don W.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Plus End-Directed Microtubule Motor Required for
; FILE REFERENCE: 18557C-000110US
; CURRENT APPLICATION NUMBER: US/09/150,867
; CURRENT FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: US 60/058,645
; EARLIER FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 9626
; TYPE: DNA
; ORGANISM: Xenopus sp.
; FEATURE:
; OTHER INFORMATION: XCENP-B nucleotide sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (143)..(9007)
US-09-150-867-2

Query Match 67.5%; Score 16.2; DB 4; Length 9626;
Best Local Similarity 85.7%; Pred. No. 1,6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TATCAGAACTCAAGTGCAGC 21
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Db 3301 TATCAGAAACAAAGTGCAGC 3321

RESULT 12

US-09-621-976-18735
; Sequence 18735, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 18735
; LENGTH: 374
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-18735

Query Match 66.7%; Score 16; DB 4; Length 374;
Best Local Similarity 79.2%; Pred. No. 97;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TATCAGAACTCAAGTGCAGCCAT 24
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Db 172 TACGAGCACACATTCAGAGCCAT 195

RESULT 13

US-09-621-976-18740

; Sequence 18740, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 18740
; LENGTH: 406
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-18740

Query Match 66.7%; Score 16; DB 4; Length 406;
Best Local Similarity 79.2%; Pred. No. 99;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TATCAGAACTCAAGTGAGCCAT 24
DB 172 TAGCAGACACCAATTGAGCCAT 195

RESULT 14
US-09-621-976-2114
; Sequence 2114, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2114
; LENGTH: 479
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: 125..322
US-09-621-976-2114

Query Match 66.7%; Score 16; DB 4; Length 479;
Best Local Similarity 79.2%; Pred. No. 1e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TATCAGAACTCAAGTGAGCCAT 24
DB 442 TGTGAGAACTCAAAAGCAATCAT 465

RESULT 15
US-09-543-681A-81
; Sequence 81, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344

; SEQ ID NO 81
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-81

Query Match 66.7%; Score 16; DB 4; Length 666;
Best Local Similarity 79.2%; Pred. No. 1.1e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TATCAGAACTCAAGTGAGCCAT 24
DB 308 TATCGAGCCTCAAGTAGCCGCAT 331

Search completed: January 26, 2005, 13:15:21
Job time : 33.925 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 26, 2005, 13:15:32 ; Search time 170.133 Seconds
(without alignments)
810.549 Million cell updates/sec

Title: US-10-085-612A-18

Perfect score: 24

Sequence: 1 taccagaactcaagtcgagccat 24

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA:*

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- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09C_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
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- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	24	100.0	1345	10	US-09-943-115A-1
C 2	24	100.0	1345	14	US-10-146-575-3
C 3	24	100.0	1345	14	US-10-085-612-3
C 4	24	100.0	13035	15	US-10-121-960C-14
C 5	24	100.0	15185	15	US-10-121-960C-17
C 6	22.4	93.3	1012	9	US-09-957-997-4
C 7	22.4	93.3	1254	14	US-10-085-612-4
C 8	22.4	93.3	1186	9	US-09-957-997-1
C 9	18.8	78.3	188	9	US-09-783-550-11156
C 10	18.4	76.7	673	18	US-10-653-047-6542
C 11	17.8	74.2	456	17	US-10-437-963-48048
C 12	17.8	74.2	556	9	US-09-917-800A-985

C 13	17.8	74.2	2724	17	US-10-437-963-48046	Sequence 48046, A
C 14	17.6	73.3	4042	15	US-10-128-714-347	Sequence 347, App
C 15	17.6	73.3	4043	15	US-10-128-714-5347	Sequence 5347, Ap
C 16	17.4	72.5	276	9	US-09-864-761-18789	Sequence 18789, A
C 17	17.4	72.5	465	9	US-09-864-761-2044	Sequence 2044, Ap
C 18	17.4	72.5	636	13	US-10-027-632-264198	Sequence 264198, A
C 19	17.4	72.5	636	15	US-10-027-632-264198	Sequence 191, App
C 20	17.2	71.7	398	10	US-09-854-867-191	Sequence 264198, A
C 21	17.2	71.7	490	15	US-10-102-524-504	Sequence 504, App
C 22	17.2	71.7	517	13	US-10-027-632-77419	Sequence 77419, A
C 23	17.2	71.7	517	13	US-10-027-632-314056	Sequence 314056, A
C 24	17.2	71.7	517	15	US-10-027-632-314056	Sequence 77419, A
C 25	17.2	71.7	517	15	US-10-027-632-314056	Sequence 314056, A
C 26	17.2	71.7	532	15	US-10-102-524-1796	Sequence 1796, Ap
C 27	17.2	71.7	615	13	US-10-027-632-225776	Sequence 225776, A
C 28	17.2	71.7	615	15	US-10-027-632-225776	Sequence 225776, A
C 29	17.2	71.7	628	18	US-10-425-115-60396	Sequence 60396, A
C 30	17.2	71.7	673	13	US-10-027-632-219635	Sequence 219635, A
C 31	17.2	71.7	673	13	US-10-027-632-219636	Sequence 219636, A
C 32	17.2	71.7	673	13	US-10-027-632-219637	Sequence 219637, A
C 33	17.2	71.7	673	15	US-10-027-632-219635	Sequence 219635, A
C 34	17.2	71.7	673	15	US-10-027-632-219636	Sequence 219636, A
C 35	17.2	71.7	673	15	US-10-027-632-219637	Sequence 219637, A
C 36	17.2	71.7	1238	16	US-10-424-599-12818	Sequence 12818, A
C 37	17.2	71.7	1281	16	US-10-424-599-12818	Sequence 43984, A
C 38	17.2	71.7	1370	18	US-09-739-930-4661	Sequence 4661, Ap
C 39	16.8	70.0	534	15	US-09-818-995-22886	Sequence 22886, A
C 40	16.8	70.0	534	15	US-10-029-386-9254	Sequence 9254, Ap
C 41	16.8	70.0	549	9	US-09-867-550-1091	Sequence 1091, Ap
C 42	16.8	70.0	584	13	US-10-027-632-186339	Sequence 186339, A
C 43	16.8	70.0	584	15	US-10-027-632-186340	Sequence 186340, A
C 44	16.8	70.0	584	15	US-10-027-632-186339	Sequence 186339, A
C 45	16.8	70.0	584	15	US-10-027-632-186340	Sequence 186340, A

ALIGNMENTS

RESULT 1
US-09-943-115A-1/c
Sequence 1, Application US/09943115A
Publication No. US20030017469A1
GENERAL INFORMATION:
APPLICANT: SEQUENOM, Inc.
APPLICANT: Rieinger, Carl
APPLICANT: Anderson, Maria
APPLICANT: Lewander, Tommy
APPLICANT: Olaisson, Erik
TITLE OF INVENTION: DETECTION OF CYP3A4 AND CYP2C9
FILE REFERENCE: 52459-20021.00
CURRENT APPLICATION NUMBER: US/09/943.115A
CURRENT FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: UK 0021286.0
PRIOR FILING DATE: 2000-08-30
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1345
TYPE: DNA
ORGANISM: Homo sapiens
US-09-943-115A-1

Query Match 100.0%; Score 24; DB 10; Length 1345;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 TATCAGAATCAAGTCGAGCCAT 24
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Db 870 TATCAGAATCAAGTCGAGCCAT 847

RESULT 2

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US-10-146-575-3/c
; Sequence 3, Application US/10146575
; Publication No. US20030059800A1
; GENERAL INFORMATION:
; APPLICANT: Lichter, Jay
; APPLICANT: Guido, Marco
; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
; FILE REFERENCE: SEQ-12P
; CURRENT APPLICATION NUMBER: US/10/146, 575
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US/09/144,367
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: Other
; LOCATION: (0)...(0)
US-10-146-575-3
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Query Match          100.0%; Score 24; DB 14; Length 1345;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      1 TATCAGAACTCAAGTGAGCCAT 24
Db      870 TATCAGAACTCAAGTGAGCCAT 847
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RESULT 3
US-10-085-612-3/c
; Sequence 3, Application US/10085612
; Publication No. US20030096251A1
; GENERAL INFORMATION:
; APPLICANT: Guida, Marco
; APPLICANT: Hall, Jeff
; APPLICANT: Petros, William
; APPLICANT: Vredenburgh, James
; APPLICANT: Colvin, Oliver
; APPLICANT: Marks, Jeffrey
; TITLE OF INVENTION: Methods for Evaluating the Ability to Metabolize Pharmaceuticals
; FILE REFERENCE: 4389-5-C1
; CURRENT APPLICATION NUMBER: US/10/085,612
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/144,367
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/271,630
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-612-3
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Query Match          100.0%; Score 24; DB 14; Length 1345;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      1 TATCAGAACTCAAGTGAGCCAT 24
Db      870 TATCAGAACTCAAGTGAGCCAT 847
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RESULT 4
US-10-121-960C-14/c
; Sequence 14, Application US/10121960C
; Publication No. US20030145341A1
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; GENERAL INFORMATION:
; APPLICANT: ZHANG, Weisheng
; APPLICANT: CONTAG, Pamela
; APPLICANT: PURCHIO, Anthony
; APPLICANT: HASHIMA, Sandy
; APPLICANT: MA, Shitley
; TITLE OF INVENTION: ISOLATION AND IDENTIFICATION OF MOUSE AND HUMAN
; TITLE OF INVENTION: TRANSCRIPTION CONTROL ELEMENTS ASSOCIATED WITH
; FILE REFERENCE: 9400-0014 / PXE-014.US
; CURRENT APPLICATION NUMBER: US/10/121,960C
; CURRENT FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 13035
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human CYP3A4 gene locus
US-10-121-960C-14
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Query Match          100.0%; Score 24; DB 15; Length 13035;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      1 TATCAGAACTCAAGTGAGCCAT 24
Db      12695 TATCAGAACTCAAGTGAGCCAT 12672
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```
RESULT 5
US-10-121-960C-17/c
; Sequence 17, Application US/10121960C
; Publication No. US20030145341A1
; GENERAL INFORMATION:
; APPLICANT: ZHANG, Weisheng
; APPLICANT: CONTAG, Pamela
; APPLICANT: PURCHIO, Anthony
; APPLICANT: HASHIMA, Sandy
; APPLICANT: MA, Shitley
; APPLICANT: NAMOTKA, Kevin
; TITLE OF INVENTION: ISOLATION AND IDENTIFICATION OF MOUSE AND HUMAN
; TITLE OF INVENTION: TRANSCRIPTION CONTROL ELEMENTS ASSOCIATED WITH
; FILE REFERENCE: 9400-0014 / PXE-014.US
; CURRENT APPLICATION NUMBER: US/10/121,960C
; CURRENT FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 15185
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CYP3A4-luc transgene
US-10-121-960C-17
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Query Match          100.0%; Score 24; DB 15; Length 15185;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      1 TATCAGAACTCAAGTGAGCCAT 24
Db      12695 TATCAGAACTCAAGTGAGCCAT 12672
```

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RESULT 6
US-09-957-997-4/c
; Sequence 4, Application US/09957997
; Patent No. US20020150915A1
; GENERAL INFORMATION:
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APPLICANT: Berkenstam, Anders
APPLICANT: Bertilsson, Gran
APPLICANT: Blomquist, Patrik
TITLE OF INVENTION: PROMOTER SEQUENCES
FILE REFERENCE: 13425-046001
CURRENT APPLICATION NUMBER: US/09/957,997
CURRENT FILING DATE: 2001-09-21
EARLIER APPLICATION NUMBER: SE 0003393-6
EARLIER FILING DATE: 2000-09-22
EARLIER APPLICATION NUMBER: 60/238,895
EARLIER FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 1012
TYPE: DNA
ORGANISM: Homo sapiens
US-09-957-997-4

Query Match 93.3%; Score 22.4; DB 9; Length 1012;
Best Local Similarity 95.8%; Pred. No. 0.97;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TATCAGAACTCAAGTGAGCCAT 24
Db 783 TATCAGAACTCAAGTGAGCCAT 760

RESULT 7
US-10-085-612-4/c
Sequence 4, Application US/10085612
Publication No. US20030096251A1

GENERAL INFORMATION:
APPLICANT: Guida, Marco
APPLICANT: Hall, Jeff
APPLICANT: Petros, William
APPLICANT: Vredenburg, James
APPLICANT: Colvin, Oliver
APPLICANT: Marks, Jeffrey
TITLE OF INVENTION: Methods for Evaluating the Ability to Metabolize Pharmaceuticals
FILE REFERENCE: 4389-5-C1
CURRENT APPLICATION NUMBER: US/10/085,612
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 09/144,367
PRIOR FILING DATE: 1998-08-31
PRIOR APPLICATION NUMBER: 60/271,630
PRIOR FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 1254
TYPE: DNA
ORGANISM: Homo sapiens
US-10-085-612-4

Query Match 93.3%; Score 22.4; DB 14; Length 1254;
Best Local Similarity 95.8%; Pred. No. 1;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TATCAGAACTCAAGTGAGCCAT 24
Db 905 TATCAGAACTCAAGTGAGCCAT 882

RESULT 8
US-09-957-997-1/c
Sequence 1, Application US/09957997
Patent No. US20020150915A1
GENERAL INFORMATION:
APPLICANT: Berkenstam, Anders
APPLICANT: Bertilsson, Gran
APPLICANT: Blomquist, Patrik

TITLE OF INVENTION: PROMOTER SEQUENCES
FILE REFERENCE: 13425-046001
CURRENT APPLICATION NUMBER: US/09/957,997
CURRENT FILING DATE: 2001-09-21
EARLIER APPLICATION NUMBER: SE 0003393-6
EARLIER FILING DATE: 2000-09-22
EARLIER APPLICATION NUMBER: 60/238,895
EARLIER FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1186
TYPE: DNA
ORGANISM: Homo sapiens
US-09-957-997-1

Query Match 93.3%; Score 22.4; DB 9; Length 1186;
Best Local Similarity 95.8%; Pred. No. 1.4;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TATCAGAACTCAAGTGAGCCAT 24
Db 10900 TATCAGAACTCAAGTGAGCCAT 10877

RESULT 9
US-09-783-590-11156

Sequence 11156, Application US/09783590
Patent No. US20020110850A1
GENERAL INFORMATION:
APPLICANT: Dillon, Patrick J.
APPLICANT: Haseltine, William A.
APPLICANT: Li, Haodong
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven W.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REFERENCE: PO-16.2C1
CURRENT APPLICATION NUMBER: US/09/783,590
CURRENT FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
PRIOR APPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11156
LENGTH: 188
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (52)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (66)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (85)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (133)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (176)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (188)
OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-11156

Query Match 78.3%; Score 18.8; DB 9; Length 188;
Best Local Similarity 87.0%; Pred. No. 43;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Mu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 48046
LENGTH: 2724
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_50759C.1
US-10-437-963-48046

Query Match 74.2%; Score 17.6; DB 15; Length 2724;
Best Local Similarity 90.5%; Pred. No. 2e+02; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 2;

QY 4 CAGAACTCAAGTGCAGCCAT 24
DB 2537 CAGAACTCAAGTGCAGCCAT 2557

RESULT 14
US-10-128-714-347/c
Sequence 347, Application US/10128714
Publication No. US20030119013A1
GENERAL INFORMATION:
APPLICANT: Jiang, Bo
APPLICANT: Hu, Wengqi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Erosbkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
FILE REFERENCE: 10182-018-999
CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
SOFTWARE: PatentIn version 3.1
SEQ ID NO 347
LENGTH: 4042
TYPE: DNA
ORGANISM: Aspergillus fumigatus
US-10-128-714-347

Query Match 73.3%; Score 17.6; DB 15; Length 4042;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TATCAGAACTCAAGTGCAGCCAT 24
DB 3941 TATCAGAACTCAAGTGCAGCCAT 3918

RESULT 15

US-10-128-714-5347/c
Sequence 5347, Application US/10128714
Publication No. US20030119013A1
GENERAL INFORMATION:
APPLICANT: Jiang, Bo
APPLICANT: Hu, Wengqi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Erosbkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
FILE REFERENCE: 10182-018-999
CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5347
LENGTH: 4043
TYPE: DNA
ORGANISM: Aspergillus fumigatus
US-10-128-714-5347

Query Match 73.3%; Score 17.6; DB 15; Length 4043;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TATCAGAACTCAAGTGCAGCCAT 24
DB 3942 TATCAGAACTCAAGTGCAGCCAT 3919

Search completed: January 26, 2005, 18:15:47
Job time: 171.133 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 26, 2005, 11:30:01 : Search time 25.9667 Seconds
(without alignments)
520.089 Million cell updates/sec

Title: US-10-085-612A-21

Sequence: 1 ggcgtgtgcattcttgc 19

Scoring table: IDENTITY NUC

Gap 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16.4	86.3	1345	US-09-372-339-1	Sequence 1, Appli
2	16.4	86.3	1345	US-09-372-339-2	Sequence 2, Appli
3	16.4	86.3	1345	US-09-144-367-3	Sequence 3, Appli
4	15.8	83.2	5722	US-09-566-921-54	Sequence 54, Appli
5	15.8	83.2	5722	US-09-919-039-174	Sequence 174, Appli
6	14.8	77.9	132	US-09-513-999C-16924	Sequence 16924, A
7	14.8	77.9	402	US-09-513-999C-16738	Sequence 16738, A
8	14.8	77.9	1617	US-08-540-118-2	Sequence 2, Appli
9	14.8	77.9	1617	US-09-185-818-2	Sequence 2, Appli
10	14.8	77.9	49312	US-09-671-317-485	Sequence 485, App
11	14.4	75.8	250	US-09-513-999C-18974	Sequence 18974, A
12	14.4	75.8	451	US-09-702-705-1647	Sequence 1647, Ap
13	14.4	75.8	451	US-09-736-457-1647	Sequence 1647, Ap
14	14.4	75.8	451	US-09-614-124B-1647	Sequence 1647, Ap
15	14.4	75.8	451	US-09-671-325-1647	Sequence 1647, Ap
16	14.4	75.8	451	US-09-658-824-1647	Sequence 1647, Ap
17	14.4	75.8	2820	US-09-540-236-479	Sequence 479, App
18	14.4	75.8	2932	US-08-999-774A-5	Sequence 5, Appli
19	14.4	75.8	2932	US-09-149-476-165	Sequence 165, App
20	14.4	75.8	3276	US-09-149-476-298	Sequence 298, App
21	14.4	75.8	3447	US-09-221-017B-816	Sequence 816, App
22	14.4	75.8	3768	US-09-566-921-50	Sequence 50, Appli
23	14.4	75.8	41684	US-09-538-059-1	Sequence 1, Appli
24	14.4	75.8	65792	US-09-536-002-31	Sequence 31, Appli
25	14.4	75.8	162450	US-09-345-882-1	Sequence 2676, Ap
26	14.2	74.7	67	US-08-956-171E-2676	Sequence 2676, Ap
27	14.2	74.7	67	US-08-761-986A-2676	Sequence 2676, Ap

28	14.2	74.7	378	US-09-702-705-1495	Sequence 1495, Ap
29	14.2	74.7	378	US-09-736-457-1495	Sequence 1495, Ap
30	14.2	74.7	378	US-09-614-124B-1495	Sequence 1495, Ap
31	14.2	74.7	378	US-09-671-325-1495	Sequence 1495, Ap
32	14.2	74.7	378	US-09-658-824-1495	Sequence 1495, Ap
33	14.2	74.7	393	US-09-134-000C-45	Sequence 45, Appli
34	14.2	74.7	407	US-09-401-064-174	Sequence 174, App
35	14.2	74.7	420	US-09-252-991A-6401	Sequence 6401, App
36	14.2	74.7	433	US-09-513-999C-1943	Sequence 1943, Ap
37	14.2	74.7	442	US-09-513-999C-9621	Sequence 9621, Ap
38	14.2	74.7	630	US-08-117-981-5	Sequence 5, Appli
39	14.2	74.7	630	US-08-477-081-5	Sequence 5, Appli
40	14.2	74.7	630	PCT-US93-02142-5	Sequence 5, Appli
41	14.2	74.7	705	US-09-107-532A-1163	Sequence 1163, Ap
42	14.2	74.7	756	US-09-270-767-88	Sequence 88, Appli
43	14.2	74.7	756	US-09-270-767-15370	Sequence 15370, A
44	14.2	74.7	845	US-08-589-446-3	Sequence 3, Appli
45	14.2	74.7	845	US-08-444-882-3	Sequence 3, Appli

ALIGNMENTS

```
RESULT 1
US-09-372-339-1
: Sequence 1, Application US/09372339
: Patent No. 6174684
: GENERAL INFORMATION:
: APPLICANT: Redbeck, Timothy
: APPLICANT: Felix, Carolyn
: TITLE OF INVENTION: CYP3A4 NFSE Variant and Methods of Use Therefor
: FILE REFERENCE: PNN-0695
: CURRENT APPLICATION NUMBER: US/09/372,339
: EARLIER FILING DATE: 1999-08-11
: EARLIER APPLICATION NUMBER: 60/096,586
: EARLIER FILING DATE: 1998-08-14
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 1345
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-372-339-1

Query Match      86.3%   Score 16.4;   DB 3;   Length 1345;
Best Local Similarity 94.4%   Pred. No. 14;
Matches 17;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

Cy      2 GTGTGTGCGATTCTTTC 19
Db      963 GTGTGTGATTCTTTC 980

RESULT 2
US-09-372-339-2
: Sequence 2, Application US/09372339
: Patent No. 6174684
: GENERAL INFORMATION:
: APPLICANT: Redbeck, Timothy
: APPLICANT: Felix, Carolyn
: TITLE OF INVENTION: CYP3A4 NFSE Variant and Methods of Use Therefor
: FILE REFERENCE: PNN-0695
: CURRENT APPLICATION NUMBER: US/09/372,339
: EARLIER FILING DATE: 1999-08-11
: EARLIER APPLICATION NUMBER: 60/096,586
: EARLIER FILING DATE: 1998-08-14
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 2
: LENGTH: 1345
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-372-339-2
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Query Match 86.3%; Score 16.4; DB 3; Length 1345;
Best Local Similarity 94.4%; Pred. No. 14;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTGTGTCGATCTTTGC 19
|||||
Db 963 GTGTGTCGATCTTTGC 980

RESULT 3
US-09-144-367-3
; Sequence 3, Application US/09144367
; Patent No. 6432639
; GENERAL INFORMATION:
; APPLICANT: Lichter, Jay
; APPLICANT: Guido, Marco
; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
; FILE REFERENCE: SEQ-12P
; CURRENT APPLICATION NUMBER: US/09/144,367
; CURRENT FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/058,612
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: Other
; LOCATION: (0)...(0)
US-09-144-367-3

Query Match 86.3%; Score 16.4; DB 4; Length 1345;
Best Local Similarity 94.4%; Pred. No. 14;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTGTGTCGATCTTTGC 19
|||||
Db 963 GTGTGTCGATCTTTGC 980

RESULT 4
US-09-566-921-54/c
; Sequence 54, Application US/09566921
; Patent No. 6682888
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tingley, Debora W.
; APPLICANT: Edwards, Carla M.
; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
; FILE REFERENCE: PA-0024 US
; CURRENT APPLICATION NUMBER: US/09/566,921
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PERL Program
; SEQ ID NO 54
; LENGTH: 5722
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6682888 331485.3
US-09-566-921-54

Query Match 83.2%; Score 15.8; DB 4; Length 5722;
Best Local Similarity 89.5%; Pred. No. 37;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTGTGTCGATCTTTGC 19
|||||
Db 5399 GGTGTGTCGATCTTTGC 5381

RESULT 5
US-09-919-039-174/c
; Sequence 174, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 174
; LENGTH: 5722
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6727066 113580.4
US-09-919-039-174

Query Match 83.2%; Score 15.8; DB 4; Length 5722;
Best Local Similarity 89.5%; Pred. No. 37;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTGTGTCGATCTTTGC 19
|||||
Db 5399 GGTGTGTCGATCTTTGC 5381

RESULT 6
US-09-513-999C-16924
; Sequence 16924, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclet, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 16924
; LENGTH: 132
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-16924

Query Match 77.9%; Score 14.8; DB 4; Length 132;
Best Local Similarity 88.9%; Pred. No. 73;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTGTGTCGATCTTTG 18
|||||
Db 55 GGTGTGTCGATCTTTG 72

RESULT 7
US-09-513-999C-16738/c
; Sequence 16738, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclet, A.

APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513.999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 16738
LENGTH: 402
TYPE: DNA
ORGANISM: Homo sapiens
US-09-513-999C-16738

Query Match 77.9%; Score 14.8; DB 4; Length 402;
Best Local Similarity 88.9%; Pred. No. 86;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTGTGCGACTTCTTTC 18
DB 147 GGTGTGCGACTTCTTTC 130

RESULT 8
US-08-540-118-2/c
Sequence 2, Application US/08540118
Patent No. 5874526
GENERAL INFORMATION:
APPLICANT: Koelen, Marcus J.M.
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: New Toxoplasma gondii antigens
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Akzo No. 5874526el Patent Department
STREET: 1300 Piccard Drive, Suite 206
CITY: Rockville
STATE: Maryland
COUNTRY: U.S.A.
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/540.118
FILING DATE: 06-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 942028994
FILING DATE: 06-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Gormley, Mary E.
REGISTRATION NUMBER: 34,409
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 258-5200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1617 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Toxoplasma gondii
STRAIN: RH
IMMEDIATE SOURCE:
CLONE: #114
US-08-540-118-2

Query Match 77.9%; Score 14.8; DB 2; Length 1617;
Best Local Similarity 88.9%; Pred. No. 1,1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTGTGCGACTTCTTTC 19
DB 1385 GTGTGCGACTTCTTTC 1368

RESULT 9
US-09-185-818-2/c
Sequence 2, Application US/09185818
Patent No. 6420540
GENERAL INFORMATION:
APPLICANT: Koelen, Marcus J.M.
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: New Toxoplasma gondii antigens
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Akzo No. 6420540el Patent Department
STREET: 1300 Piccard Drive, Suite 206
CITY: Rockville
STATE: Maryland
COUNTRY: U.S.A.
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/185.818
FILING DATE: 04-NOV-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/540.118
FILING DATE: 06-OCT-1995
APPLICATION NUMBER: EP 942028994
FILING DATE: 06-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Gormley, Mary E.
REGISTRATION NUMBER: 34,409
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 258-5200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1617 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Toxoplasma gondii
STRAIN: RH
IMMEDIATE SOURCE:
CLONE: #114
US-09-185-818-2

Query Match 77.9%; Score 14.8; DB 4; Length 1617;
Best Local Similarity 88.9%; Pred. No. 1,1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTGTGCGACTTCTTTC 19
DB 1385 GTGTGCGACTTCTTTC 1368

RESULT 10
US-09-671-317-485
Sequence 485, Application US/09671317
Patent No. 6528260
GENERAL INFORMATION:

APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
APPLICANT: Bougueleret, Lydie
APPLICANT: Cohen, Amick
TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
FILE REFERENCE: 62.US3.CIP
CURRENT APPLICATION NUMBER: US/09/671,317
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 09/536,178
PRIOR FILING DATE: 2000-03-23
PRIOR APPLICATION NUMBER: PCT/IB00/00403
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: US 60/126,269
PRIOR FILING DATE: 1999-03-25
PRIOR APPLICATION NUMBER: US 60/131,961
PRIOR FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 977
SOFTWARE: Patent.pm
SEQ ID NO 485
LENGTH: 49312
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 5466..7466
OTHER INFORMATION: 5:regulatory region
NAME/KEY: exon
LOCATION: 7467..7725
OTHER INFORMATION: exon 1
NAME/KEY: exon
LOCATION: 20256..20355
OTHER INFORMATION: exon 2
NAME/KEY: exon
LOCATION: 36905..36975
OTHER INFORMATION: exon 3
NAME/KEY: exon
LOCATION: 45167..45248
OTHER INFORMATION: exon 4
NAME/KEY: exon
LOCATION: 45728..45965
OTHER INFORMATION: exon 5
NAME/KEY: misc feature
LOCATION: 45966..49312
OTHER INFORMATION: 3:regulatory region
NAME/KEY: allele
LOCATION: 7564
OTHER INFORMATION: 10-286-289 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 7619
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NAME/KEY: allele
LOCATION: 7649
OTHER INFORMATION: 10-286-375 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 17258
OTHER INFORMATION: 12-425-57 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 21590
OTHER INFORMATION: 12-421-135 : insertion of T
NAME/KEY: allele
LOCATION: 21595
OTHER INFORMATION: 12-421-140 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 36971
OTHER INFORMATION: 10-523-232 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 45214
OTHER INFORMATION: 10-289-201 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 45741
OTHER INFORMATION: 10-290-37 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 46029

OTHER INFORMATION: 10-290-326 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 46032
OTHER INFORMATION: 10-290-328 : deletion of G
NAME/KEY: primer bind
LOCATION: 7276..7294
OTHER INFORMATION: 10-286.pu
NAME/KEY: primer bind
LOCATION: 7676..7694
OTHER INFORMATION: 10-286.rp complement
NAME/KEY: primer bind
LOCATION: 16839..16856
OTHER INFORMATION: 12-425.rp
NAME/KEY: primer bind
LOCATION: 17297..17314
OTHER INFORMATION: 12-425.pu complement
NAME/KEY: primer bind
LOCATION: 21456..21474
OTHER INFORMATION: 12-421.pu
NAME/KEY: primer bind
LOCATION: 21886..21906
OTHER INFORMATION: 12-421.rp complement
NAME/KEY: primer bind
LOCATION: 36740..36758
OTHER INFORMATION: 10-523.pu
NAME/KEY: primer bind
LOCATION: 36997..37015
OTHER INFORMATION: 10-523.rp complement
NAME/KEY: primer bind
LOCATION: 45020..45037
OTHER INFORMATION: 10-289.pu
NAME/KEY: primer bind
LOCATION: 45413..45432
OTHER INFORMATION: 10-289.rp complement
NAME/KEY: primer bind
LOCATION: 45705..45724
OTHER INFORMATION: 10-290.pu
NAME/KEY: primer bind
LOCATION: 46104..46123
OTHER INFORMATION: 10-290.rp complement
NAME/KEY: primer bind
LOCATION: 7545..7563
OTHER INFORMATION: 10-286-289.mis
NAME/KEY: primer bind
LOCATION: 7565..7583
OTHER INFORMATION: 10-286-289.mis complement
NAME/KEY: primer bind
LOCATION: 7600..7618
OTHER INFORMATION: 10-286-345.mis
NAME/KEY: primer bind
LOCATION: 7620..7638
OTHER INFORMATION: 10-286-345.mis complement
NAME/KEY: primer bind
LOCATION: 7630..7648
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NAME/KEY: primer bind
LOCATION: 7650..7668
OTHER INFORMATION: 10-286-375.mis complement
NAME/KEY: primer bind
LOCATION: 17239..17257
OTHER INFORMATION: 12-425-57.mis
NAME/KEY: primer bind
LOCATION: 17259..17277
OTHER INFORMATION: 12-425-57.mis complement
NAME/KEY: primer bind
LOCATION: 21596..21614
OTHER INFORMATION: 12-421-140.mis
NAME/KEY: primer bind
LOCATION: 36952..36970
OTHER INFORMATION: 10-523-232.mis

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NAME/KEY: primer_bind
LOCATION: 36972..36990
OTHER INFORMATION: 10-523-232.mis complement
NAME/KEY: primer_bind
LOCATION: 45195..45213
OTHER INFORMATION: 10-289-201.mis
NAME/KEY: primer_bind
LOCATION: 45215..45233
OTHER INFORMATION: 10-289-201.mis complement
NAME/KEY: primer_bind
LOCATION: 45722..45740
OTHER INFORMATION: 10-290-37.mis
NAME/KEY: primer_bind
LOCATION: 45742..45760
OTHER INFORMATION: 10-290-37.mis complement
NAME/KEY: primer_bind
LOCATION: 46010..46028
OTHER INFORMATION: 10-290-326.mis
NAME/KEY: primer_bind
LOCATION: 46030..46048
OTHER INFORMATION: 10-290-326.mis complement
NAME/KEY: misc_binding
LOCATION: 7352..7576
OTHER INFORMATION: 10-286-289.probe
NAME/KEY: misc_binding
LOCATION: 7607..7631
OTHER INFORMATION: 10-286-345.probe
NAME/KEY: misc_binding
LOCATION: 7637..7661
OTHER INFORMATION: 10-286-375.probe
NAME/KEY: misc_binding
LOCATION: 17246..17270
OTHER INFORMATION: 12-425-57.probe
NAME/KEY: misc_binding
LOCATION: 21583..21607
OTHER INFORMATION: 12-421-140.probe
NAME/KEY: misc_binding
LOCATION: 36959..36983
OTHER INFORMATION: 10-523-232.probe
NAME/KEY: misc_binding
LOCATION: 45202..45226
OTHER INFORMATION: 10-289-201.probe
NAME/KEY: misc_binding
LOCATION: 45729..45753
OTHER INFORMATION: 10-290-37.probe
NAME/KEY: misc_binding
LOCATION: 46017..46041
OTHER INFORMATION: 10-290-326.probe
US-09-671-317-485
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Query Match 77.8%; Score 14.8; DB 4; Length 49312;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTGTGTCGATTCCTTGC 19
DB 16640 GTGTGTCGATTCCTTGC 16657

RESULT 11
US-09-513-999C-18974
Sequence 18974, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J. B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J. Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513.999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
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PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 18974
LENGTH: 250
TYPE: DNA
ORGANISM: Homo sapiens
US-09-513-999C-18974
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Query Match 75.8%; Score 14.4; DB 4; Length 250;
Best Local Similarity 93.8%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 190 GTGTGTCGATTCCTT 205
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RESULT 12
US-09-702-705-1647/c
Sequence 1647, Application US/09702705
Patent No. 6504010
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaltanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.478C14
CURRENT APPLICATION NUMBER: US/09/702.705
CURRENT FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 1833
SOFTWARE: PaetsSeq for Windows Version 3.0
SEQ ID NO 1647
LENGTH: 451
TYPE: DNA
ORGANISM: Homo sapiens
US-09-702-705-1647
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Query Match 75.8%; Score 14.4; DB 4; Length 451;
Best Local Similarity 93.8%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 3 TGTGTGCTATTCCTTG 18
DB 379 TGTGTGCTATTCCTTG 364
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RESULT 13
US-09-736-457-1647/c
Sequence 1647, Application US/09736457
Patent No. 6509448
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaltanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Pan, Liqun
APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.478C15
CURRENT APPLICATION NUMBER: US/09/736.457
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; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1647
; LENGTH: 451
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-736-457-1647

Query Match
Best Local Similarity 75.8%; Score 14.4; DB 4; Length 451;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGTGTGCGATTCTTTG 18
Db 379 TGTGTGCTATTCTTTG 364

RESULT 14
US-09-614-124B-1647/c
; Sequence 1647, Application US/09614124B
; Patent No. 6630574
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.478C9
; CURRENT APPLICATION NUMBER: US/09/614,124B
; NUMBER OF SEQ ID NOS: 1668
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1647
; LENGTH: 451
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-614-124B-1647

Query Match
Best Local Similarity 75.8%; Score 14.4; DB 4; Length 451;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGTGTGCGATTCTTTG 18
Db 379 TGTGTGCTATTCTTTG 364

RESULT 15
US-09-671-325-1647/c
; Sequence 1647, Application US/09671325
; Patent No. 6667154
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C12
; CURRENT APPLICATION NUMBER: US/09/671,325
; CURRENT FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 1825
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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1647
; LENGTH: 451
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-671-325-1647

Query Match
Best Local Similarity 75.8%; Score 14.4; DB 4; Length 451;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGTGTGCGATTCTTTG 18
Db 379 TGTGTGCTATTCTTTG 364

Search completed: January 26, 2005, 13:15:22
Job time : 27.0917 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 26, 2005, 13:15:32 ; Search time 134.689 Seconds
(without alignments)
810.549 Million cell updates/sec

Title: US-10-085-612A-21

Perfect score: 19

Sequence: 1 ggcgtgcgcattcttgc 19

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues 8600550

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Listing first 45 summaries

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Published Applications NA:*

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21: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	16.4	86.3	1345	14	US-09-943-115A-1
3	16.4	86.3	1345	14	US-10-146-575-3
4	16.4	86.3	1345	14	US-10-085-612-3
5	16.4	86.3	1345	14	US-10-257-166-149
6	16.4	86.3	13035	15	US-10-121-960C-14
7	16.4	86.3	15185	15	US-10-121-960C-17
8	15.8	83.2	225	15	US-10-098-2638-23844
9	15.8	83.2	50	16	US-10-252-287-3
10	15.8	83.2	50	16	US-10-252-287-4
11	15.8	83.2	191	18	US-10-425-115-174784
12	15.8	83.2	322	9	US-09-960-352-11673

13	15.8	83.2	581	13	US-10-027-632-19705	Sequence 19705, A
14	15.8	83.2	581	13	US-10-027-632-19705	Sequence 19705, A
15	15.8	83.2	720	13	US-10-027-632-155127	Sequence 155127, A
16	15.8	83.2	720	13	US-10-027-632-155127	Sequence 155127, A
17	15.8	83.2	2000	9	US-09-938-842A-3958	Sequence 3958, Ap
18	15.8	83.2	2000	11	US-09-938-842A-3958	Sequence 3958, Ap
19	15.8	83.2	5722	10	US-09-919-039-174	Sequence 174, App
20	15.8	83.2	6487	18	US-10-335-053-159	Sequence 159, App
21	15.4	81.1	366	9	US-09-960-352-10415	Sequence 10415, A
22	15.4	81.1	414	9	US-09-960-352-10901	Sequence 10901, A
23	15.4	81.1	493	10	US-09-918-995-17875	Sequence 17875, A
24	14.8	77.9	162	18	US-10-674-124A-9954	Sequence 9954, Ap
25	14.8	77.9	230	18	US-10-425-115-127551	Sequence 127551, A
26	14.8	77.9	294	17	US-10-437-963-17881	Sequence 17881, A
27	14.8	77.9	301	18	US-10-425-115-41613	Sequence 41613, A
28	14.8	77.9	372	10	US-09-803-719-797	Sequence 797, App
29	14.8	77.9	386	18	US-10-674-124A-6241	Sequence 6241, Ap
30	14.8	77.9	388	9	US-09-960-352-10766	Sequence 10766, A
31	14.8	77.9	427	18	US-10-674-124A-6240	Sequence 6240, Ap
32	14.8	77.9	468	13	US-10-027-632-300031	Sequence 300031, A
33	14.8	77.9	468	15	US-10-027-632-300031	Sequence 300031, A
34	14.8	77.9	471	17	US-10-437-963-59066	Sequence 59066, A
35	14.8	77.9	492	16	US-10-276-774-299	Sequence 299, App
36	14.8	77.9	553	13	US-10-027-632-191054	Sequence 191054, A
37	14.8	77.9	553	13	US-10-027-632-191055	Sequence 191055, A
38	14.8	77.9	553	15	US-10-027-632-191054	Sequence 191054, A
39	14.8	77.9	553	15	US-10-027-632-191055	Sequence 191055, A
40	14.8	77.9	559	13	US-10-027-632-222524	Sequence 222524, A
41	14.8	77.9	559	13	US-10-027-632-222525	Sequence 222525, A
42	14.8	77.9	559	15	US-10-027-632-222526	Sequence 222526, A
43	14.8	77.9	559	15	US-10-027-632-222525	Sequence 222525, A
44	14.8	77.9	559	15	US-10-027-632-222525	Sequence 222525, A
45	14.8	77.9	559	15	US-10-027-632-222526	Sequence 222526, A

ALIGNMENTS

RESULT 1

US-10-085-612-4

Sequence 4, Application US/10085612

Publication No. US20030096251A1

GENERAL INFORMATION:

APPLICANT: Guida, Marco

APPLICANT: Hall, Jeff

APPLICANT: Petrov, William

APPLICANT: Vredenburg, James

APPLICANT: Colvin, Oliver

APPLICANT: Marks, Jeffrey

TITLE OF INVENTION: Methods for Evaluating the Ability to Metabolize Pharmaceuticals

FILE REFERENCE: 4389-5-Cl

CURRENT APPLICATION NUMBER: US/10/085,612

CURRENT FILING DATE: 2002-02-26

PRIOR APPLICATION NUMBER: 09/144,367

PRIOR FILING DATE: 1998-08-31

PRIOR APPLICATION NUMBER: 60/271,630

PRIOR FILING DATE: 2001-02-26

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PatentIn version 3.0

SEQ ID NO 4

LENGTH: 1254

TYPE: DNA

ORGANISM: Homo sapiens

US-10-085-612-4

Query Match 100.0%; Score 19; DB 14; Length 1254;

Best Local Similarity 100.0%; Pred. No. 8.9; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-09-943-115A-1
; Sequence 1, Application US/09943115A
; Publication No. US20030017469A1
; GENERAL INFORMATION:
; APPLICANT: SEQUENOM, Inc.
; APPLICANT: Rieinger, Carl
; APPLICANT: Andersson, Maria
; APPLICANT: Lewander, Tommy
; APPLICANT: Olaisson, Erik
; TITLE OF INVENTION: DETECTION OF CYP3A4 AND CYP2C9
; FILE REFERENCE: 52459-20021.00
; CURRENT APPLICATION NUMBER: US/09/943,115A
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: UK 0021286.0
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-943-115A-1
```

```
Query Match      86.3%; Score 16.4; DB 10; Length 1345;
Best Local Similarity 94.4%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 GTGTGTCGATCTTTGC 19
      |||||
Db      963 GTGTGTGATCTTTGC 980
```

```
RESULT 3
US-10-146-575-3
; Sequence 3, Application US/10146575
; Publication No. US20030059800A1
; GENERAL INFORMATION:
; APPLICANT: Lichter, Jay
; APPLICANT: Guido, Marco
; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
; FILE REFERENCE: SEQ-12P
; CURRENT APPLICATION NUMBER: US/10/146,575
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US/09/144,367
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: Other
; LOCATION: (0)...(0)
US-10-146-575-3
```

```
Query Match      86.3%; Score 16.4; DB 14; Length 1345;
Best Local Similarity 94.4%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 GTGTGTCGATCTTTGC 19
      |||||
Db      963 GTGTGTGATCTTTGC 980
```

```
RESULT 4
US-10-085-612-3
; Sequence 3, Application US/10085612
; Publication No. US20030096251A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Guida, Marco
; APPLICANT: Hall, Jeff
; APPLICANT: Petros, William
; APPLICANT: Vredenburg, James
; APPLICANT: Colvin, Oliver
; APPLICANT: Marks, Jeffrey
; TITLE OF INVENTION: Methods for Evaluating the Ability to Metabolize Pharmaceuticals
; FILE REFERENCE: 4389-5-C1
; CURRENT APPLICATION NUMBER: US/10/085,612
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/144,367
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/271,630
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-612-3
```

```
Query Match      86.3%; Score 16.4; DB 14; Length 1345;
Best Local Similarity 94.4%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 GTGTGTCGATCTTTGC 19
      |||||
Db      963 GTGTGTGATCTTTGC 980
```

```
RESULT 5
US-10-257-166-149
; Sequence 149, Application US/10257166
; Publication No. US20040023230A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Method and Nucleic Acids for Analysing the Methylation of
; FILE REFERENCE: 5013.1011
; CURRENT APPLICATION NUMBER: US/10/257,166
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: PCT/EP01/07470
; DE 10032529.7
; DE 10043826.1
; PRIOR FILING DATE: 2001-06-29
; 2000-09-01
; 2000-06-30
; NUMBER OF SEQ ID NOS: 178
; SEQ ID NO 149
; LENGTH: 8776
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-257-166-149
```

```
Query Match      86.3%; Score 16.4; DB 16; Length 8776;
Best Local Similarity 94.4%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 GGTTGTGCGATCTTTG 18
      |||||
Db      4900 GGTTGTGCGATCTTTTG 4917
```

```
RESULT 6
US-10-121-960C-14
; Sequence 14, Application US/10121960C
```


Publication No. US20030145341A1
GENERAL INFORMATION:
APPLICANT: ZHANG, Weisheng
APPLICANT: CONTAG, Pamela
APPLICANT: PURCHIO, Anthony
APPLICANT: HASHIMA, Sandy
APPLICANT: MA, Shirley
APPLICANT: NAMOTKA, Kevin
TITLE OF INVENTION: ISOLATION AND IDENTIFICATION OF MOUSE AND HUMAN
TITLE OF INVENTION: TRANSCRIPTION CONTROL ELEMENTS ASSOCIATED WITH
TITLE OF INVENTION: CYTOCHROME EXPRESSION
FILE REFERENCE: 9400-0014 / PXE-014.US
CURRENT APPLICATION NUMBER: US/10/121,960C
CURRENT FILING DATE: 2002-04-11
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 13035
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: human CYP3A4 gene locus
US-10-121-960C-14

Query Match 86.3%; Score 16.4; DB 15; Length 13035;
Best Local Similarity 94.4%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTGTGTCGATTCCTTGC 19
DB 12788 GTGTGTCGATTCCTTGC 12805

RESULT 7
US-10-121-960C-17
Sequence 17, Application US/10121960C
Publication No. US20030145341A1
GENERAL INFORMATION:
APPLICANT: ZHANG, Weisheng
APPLICANT: CONTAG, Pamela
APPLICANT: PURCHIO, Anthony
APPLICANT: HASHIMA, Sandy
APPLICANT: MA, Shirley
APPLICANT: NAMOTKA, Kevin
TITLE OF INVENTION: ISOLATION AND IDENTIFICATION OF MOUSE AND HUMAN
TITLE OF INVENTION: TRANSCRIPTION CONTROL ELEMENTS ASSOCIATED WITH
FILE REFERENCE: 9400-0014 / PXE-014.US
CURRENT APPLICATION NUMBER: US/10/121,960C
CURRENT FILING DATE: 2002-04-11
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 15185
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: CYP3A4-luc transgene
US-10-121-960C-17

Query Match 86.3%; Score 16.4; DB 15; Length 15185;
Best Local Similarity 94.4%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTGTGTCGATTCCTTGC 19
DB 12788 GTGTGTCGATTCCTTGC 12805

RESULT 8
US-10-098-263B-23844/c
Sequence 23844, Application US/10098263B
Publication No. US20030104410A1

GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 23844
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-23844

Query Match 83.2%; Score 15.8; DB 15; Length 25;
Best Local Similarity 89.5%; Pred. No. 2.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTTGTGCGATTCCTTGC 19
DB 25 GGTTGTGCGATTCCTTGC 7

RESULT 9
US-10-252-287-3
Sequence 3, Application US/10252287
Publication No. US20040059102A1
GENERAL INFORMATION:
APPLICANT: Lucant Technologies Inc.
APPLICANT: Mills, Jr., Allen P
APPLICANT: Yurke, Bernard
TITLE OF INVENTION: COMPOSITIONS THAT REVERSIBLY GEL AND DE-GEL
FILE REFERENCE: MILLS 18-14
CURRENT APPLICATION NUMBER: US/10/252,287
CURRENT FILING DATE: 2002-11-01
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 50
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: a oligonucleotide that ser
US-10-252-287-3

Query Match 83.2%; Score 15.8; DB 16; Length 50;
Best Local Similarity 89.5%; Pred. No. 3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTTGTGCGATTCCTTGC 19
DB 26 GGTTGTGCGATTCCTTGC 44

RESULT 10
US-10-252-287-4/c
Sequence 4, Application US/10252287
Publication No. US20040059102A1
GENERAL INFORMATION:
APPLICANT: Lucant Technologies Inc.
APPLICANT: Mills, Jr., Allen P
APPLICANT: Yurke, Bernard
TITLE OF INVENTION: COMPOSITIONS THAT REVERSIBLY GEL AND DE-GEL
FILE REFERENCE: MILLS 18-14
CURRENT APPLICATION NUMBER: US/10/252,287
CURRENT FILING DATE: 2002-11-01
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 50

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: a oligonucleotide that sex
OTHER INFORMATION: ves as a removal agent for a cross-linked polyacrylamide gel
US-10-252-287-4

Query Match 83.2%; Score 15.8; DB 16; Length 50;
Best Local Similarity 89.5%; Pred. No. 3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GGTTGTGCGATTCTTTC 19
|||||
Db 25 GGTTGTGCGATTCTTTC 7

RESULT 11
US-10-425-115-174784/C
Sequence 174784, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 174784
LENGTH: 191
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MFT4577_90986C.1
US-10-425-115-174784

Query Match 83.2%; Score 15.8; DB 18; Length 191;
Best Local Similarity 89.5%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GGTTGTGCGATTCTTTC 19
|||||
Db 107 GGTTGTGCGATTCTTTC 89

RESULT 12
US-09-960-352-11673/C
Sequence 11673, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengping
APPLICANT: Byatt, John C.
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 11673
LENGTH: 322
TYPE: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 50-LIB3057-019-Q1-K1-E10
US-09-960-352-11673

Query Match 83.2%; Score 15.8; DB 9; Length 322;
Best Local Similarity 89.5%; Pred. No. 3.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GGTTGTGCGATTCTTTC 19
|||||
Db 236 GGTTGTGCGATTCTTTC 218

RESULT 13
US-10-027-632-19705
Sequence 19705, Application US/10027632
Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 19705
LENGTH: 581
TYPE: DNA
ORGANISM: Human
US-10-027-632-19705

Query Match 83.2%; Score 15.8; DB 13; Length 581;
Best Local Similarity 89.5%; Pred. No. 3.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GGTTGTGCGATTCTTTC 19
|||||
Db 399 GGTTGTGCGATTCTTTC 417

RESULT 14
US-10-027-632-19705
Sequence 19705, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 19705
 LENGTH: 581
 TYPE: DNA
 ORGANISM: Human
 US-10-027-632-19705

Query Match 83.2%; Score 15.8; DB 13; Length 581;
 Best Local Similarity 89.5%; Pred. No. 3.6e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGATGTCGATCTTGC 19
 |||||
 Db 399 GGATGTCGATCTTGC 417

RESULT 15
 US-10-027-632-155127
 ; Sequence 155127, Application US/10027632
 ; Publication No. US20020198371A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
 ; FILE REFERENCE: 108827.129
 ; CURRENT APPLICATION NUMBER: US/10/027,632
 ; CURRENT FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 60/218,006
 ; PRIOR FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: US 60/198,676
 ; PRIOR FILING DATE: 2000-04-20
 ; PRIOR APPLICATION NUMBER: US 60/193,483
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: US 60/185,218
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/167,363
 ; PRIOR FILING DATE: 1999-11-23
 ; PRIOR APPLICATION NUMBER: US 60/156,358
 ; PRIOR FILING DATE: 1999-09-28
 ; PRIOR APPLICATION NUMBER: US 60/146,002
 ; PRIOR FILING DATE: 1999-08-09
 ; NUMBER OF SEQ ID NOS: 325720
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 155127
 ; LENGTH: 720
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-10-027-632-155127

Query Match 83.2%; Score 15.8; DB 13; Length 720;
 Best Local Similarity 89.5%; Pred. No. 3.7e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGATGTCGATCTTGC 19
 |||||
 Db 540 GGATGTCGATCTTGC 558

Search completed: January 26, 2005, 18:15:48
 Job time : 135.689 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 26, 2005, 11:30:01 ; Search time 27.3333 Seconds

(without alignments)
520.089 Million cell updates/sec

Title: US-10-085-612A-22

Sequence: 1 cccgcacagcagctcttag 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PCtUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfileseq1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	17.4	87.0	1230025	4 US-09-198-452A-1	Sequence 1, Appli
2	16.8	84.0	2492	3 US-08-695-191-3	Sequence 3, Appli
3	16.8	84.0	2492	3 US-08-682-080-3	Sequence 3, Appli
4	16.8	84.0	2492	4 US-09-096-648-3	Sequence 3, Appli
5	16.8	84.0	2517	3 US-09-534-407-5	Sequence 5, Appli
6	16.8	84.0	2517	4 US-09-999-201B-2	Sequence 2, Appli
7	16.8	84.0	2517	4 US-10-281-673A-2	Sequence 2, Appli
8	15.8	79.0	1547	4 US-09-800-729-76	Sequence 76, Appli
C 9	15.4	77.0	65	1 US-08-190-687B-9	Sequence 9, Appli
C 10	15.4	77.0	3456	1 US-08-190-687B-24	Sequence 24, Appli
C 11	15.4	77.0	63000	4 US-09-786-172-18	Sequence 18, Appli
C 12	15.2	76.0	278	4 US-09-313-284A-5792	Sequence 987, Ap
C 13	15.2	76.0	286	4 US-09-313-294A-987	Sequence 987, App
C 14	15.2	76.0	328	4 US-09-023-655-471	Sequence 8, Appli
C 15	15.2	76.0	630	4 US-09-733-167A-8	Sequence 3, Appli
C 16	15.2	76.0	1045	3 US-08-859-157-3	Sequence 3, Appli
C 17	15.2	76.0	1045	3 US-09-109-273-3	Sequence 3, Appli
C 18	15.2	76.0	1045	3 US-09-276-993-3	Sequence 3, Appli
C 19	15.2	76.0	1045	3 US-09-723-450-3	Sequence 3, Appli
C 20	15.2	76.0	1142	4 US-09-733-167A-2	Sequence 2, Appli
C 21	15.2	76.0	1230	4 US-09-023-669-3	Sequence 3, Appli
C 22	15.2	76.0	1230	4 US-09-603-567-3	Sequence 3, Appli
C 23	15.2	76.0	1553	3 US-09-022-669-1	Sequence 1, Appli
C 24	15.2	76.0	1553	3 US-09-603-567-1	Sequence 1, Appli
C 25	15.2	76.0	1737	3 US-09-173-151A-1	Sequence 1, Appli
C 26	15.2	76.0	2061	3 US-09-173-151A-3	Sequence 3, Appli
C 27	15.2	76.0	16595	3 US-09-146-053-7	Sequence 7, Appli

28	15.2	76.0	48974	3 US-08-920-422-17	Sequence 17, Appli
29	15	75.0	544	4 US-09-370-838-280	Sequence 280, App
30	15	75.0	544	4 US-09-854-133-280	Sequence 280, App
31	15	75.0	5917	3 US-08-692-922-1	Sequence 1, Appli
32	15	75.0	54945	4 US-09-967-669-10	Sequence 10, Appli
C 33	14.8	74.0	71	1 US-08-400-440A-83	Sequence 83, Appli
C 34	14.8	74.0	71	1 US-08-463-093A-83	Sequence 83, Appli
C 35	14.8	74.0	71	2 US-08-460-888A-83	Sequence 83, Appli
C 36	14.8	74.0	71	2 US-08-894-578-83	Sequence 83, Appli
C 37	14.8	74.0	71	3 US-09-412-017-83	Sequence 83, Appli
C 38	14.8	74.0	322	4 US-09-513-999C-16959	Sequence 16959, A
C 39	14.8	74.0	426	4 US-09-513-999C-10945	Sequence 10945, A
40	14.8	74.0	495	4 US-09-620-312D-689	Sequence 689, App
41	14.8	74.0	510	4 US-09-621-976-18004	Sequence 18004, A
C 42	14.8	74.0	637	4 US-09-602-787A-107	Sequence 107, App
C 43	14.8	74.0	1001	4 US-09-641-638-440	Sequence 440, App
C 44	14.8	74.0	1001	4 US-10-170-097-440	Sequence 440, App
45	14.8	74.0	1140	1 US-08-348-792-11	Sequence 11, Appli

ALIGNMENTS

RESULT 1
US-09-198-452A-1/c
Sequence 1, Application US/09198452A
Patent No. 6559294
GENERAL INFORMATION:
APPLICANT: Griffiths, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevent
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 1
LENGTH: 1230025
TYPE: DNA
ORGANISM: Chlamydia pneumoniae
FEATURE:
NAME/KEY: misc feature
LOCATION: (1) ..(15000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (15001) ..(30000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (30001) ..(45000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (45001) ..(60000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (60001) ..(75000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (75001) ..(90000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (90001) ..(105000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (105001) ..(120000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (120001) ..(135000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (135001) ..(150000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (150001) ..(165000)

LOCATION: (885001)..(900000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (900001)..(915000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature

Query Match 87.0%; Score 17.4; DB 4; Length 1230025;
Best Local Similarity 94.7%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CCTGCACAGCAGCTCTTAGG 20
Db 691511 CCTGCAAGCAGCTCTTAGG 691493

RESULT 2

US-08-695-191-3

; Sequence 3, Application US/08695191

; Patent No. 6025155

GENERAL INFORMATION:

APPLICANT: Hadlaczky, Gyula

APPLICANT: Szalay, Aladar

TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF AND

TITLE OF INVENTION: METHODS FOR PREPARING ARTIFICIAL CHROMOSOMES

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Brown, Martin, Haller & McClain

STREET: 1660 Union Street

CITY: San Diego

STATE: CA

COUNTRY: USA

ZIP: 92101-2926

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/695,191

FILING DATE: 07-AUG-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE: 15-JUL-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/629,822

FILING DATE: 10-APR-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie L

REGISTRATION NUMBER: 33,779

REFERENCE/DOCKET NUMBER: 6869-402C

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-238-0999

TELEFAX: 619-238-0062

TELEX:

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 2492 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Genomic DNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE:

ORIGINAL SOURCE:

FEATURE:

Best Local Similarity 90.0%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CCTGCACAGCAGCTCTTAGG 20
Db 2082 CCTGCACAGCAGCTCTTAGG 2101

RESULT 3

US-08-682-080-3

; Sequence 3, Application US/08682080

; Patent No. 6077697

GENERAL INFORMATION:

APPLICANT: Hadlaczky, Gyula

APPLICANT: Szalay, Aladar

TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF AND METHODS FOR

TITLE OF INVENTION: PREPARING ARTIFICIAL CHROMOSOMES

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Brown, Martin, Haller & McClain

STREET: 1660 Union Street

CITY: San Diego

STATE: CA

COUNTRY: USA

ZIP: 92101-2926

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/682,080

FILING DATE: 10-APR-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/629,822

FILING DATE: 10-APR-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie L

REGISTRATION NUMBER: 33,779

REFERENCE/DOCKET NUMBER: 6869-402B

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-238-0999

TELEFAX: 619-238-0062

TELEX:

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 2492 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Genomic DNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE:

ORIGINAL SOURCE:

FEATURE:

US-08-682-080-3

Query Match 84.0%; Score 16.8; DB 3; Length 2492;
Best Local Similarity 90.0%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CCTGCACAGCAGCTCTTAGG 20
Db 2082 CCTGCACAGCAGCTCTTAGG 2101

RESULT 4

US-09-096-648-3

; Sequence 3, Application US/09096648

; Patent No. 6743967

GENERAL INFORMATION:

APPLICANT: Hadlaczky, Gyula

APPLICANT: Szalay, Aladar

TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF AND METHODS FOR

TITLE OF INVENTION: PREPARING ARTIFICIAL CHROMOSOMES

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Brown, Martin, Haller & McClain

STREET: 1660 Union Street

CITY: San Diego

STATE: CA

COUNTRY: USA

ZIP: 92101-2926

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/682,080

FILING DATE: 10-APR-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/629,822

FILING DATE: 10-APR-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie L

REGISTRATION NUMBER: 33,779

REFERENCE/DOCKET NUMBER: 6869-402B

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-238-0999

TELEFAX: 619-238-0062

TELEX:

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 2492 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Genomic DNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE:

ORIGINAL SOURCE:

FEATURE:

US-08-682-080-3

Query Match 84.0%; Score 16.8; DB 4; Length 2517;
Best Local Similarity 90.0%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTGCACAGCAGTCTTAGG 20
DB 1016 CCTGCTCAGCAGTCTGAGG 1035

RESULT 8
US-09-800-729-76
Sequence 76, Application US/09800729
Patent No. 6605592
GENERAL INFORMATION:

APPLICANT: Nt et al.
TITLE OF INVENTION: 32 Human secreted proteins
FILE REFERENCE: P2044P1
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: PCT/US00/26013
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 60/155,709
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 217
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 76
LENGTH: 1547
TYPE: DNA
ORGANISM: Homo sapiens
US-09-800-729-76

Query Match 79.0%; Score 15.8; DB 4; Length 1547;
Best Local Similarity 89.5%; Pred. No. 73;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCTGCACAGCAGTCTTAGG 20
DB 498 CCTGCACAGCAGTCTGAGG 516

RESULT 9
US-08-190-687B-9/C
Sequence 9, Application US/08190687B
Patent No. 5760203
GENERAL INFORMATION:
APPLICANT: Wong, Gail L.
APPLICANT: Martin, George
APPLICANT: McCormick, Francis P.
APPLICANT: Rubinfeld, Bonnie
APPLICANT: O'Rourke, Edward C.
APPLICANT: Clark, Robin
TITLE OF INVENTION: GAP Gene Sequences
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,687B
FILING DATE: 02-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/774,644
FILING DATE: 11-OCT-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/260,807
FILING DATE: 21-OCT-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/230,761
FILING DATE: 10-AUG-1988
ATTORNEY/AGENT INFORMATION:
NAME: Gase, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 27527/31898
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 65 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-190-687B-9

Query Match 77.0%; Score 15.4; DB 1; Length 65;
Best Local Similarity 94.1%; Pred. No. 75;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCTGCACAGCAGTCTTA 18
DB 23 CCTGAACAGCAGTCTTA 7

RESULT 10
US-08-190-687B-24/C
Sequence 24, Application US/08190687B
Patent No. 5760203
GENERAL INFORMATION:
APPLICANT: Wong, Gail L.
APPLICANT: Martin, George
APPLICANT: McCormick, Francis P.
APPLICANT: Rubinfeld, Bonnie
APPLICANT: O'Rourke, Edward C.
APPLICANT: Clark, Robin
TITLE OF INVENTION: GAP Gene Sequences
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,687B
FILING DATE: 02-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/774,644
FILING DATE: 11-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/260,807
FILING DATE: 21-OCT-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/230,761
FILING DATE: 10-AUG-1988
ATTORNEY/AGENT INFORMATION:
NAME: Gase, David A.
REGISTRATION NUMBER: 38,153

```
REFERENCE/DOCKET NUMBER: 27527/31898
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 3456 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 100..2709
US-08-190-687B-24

Query Match          77.0%; Score 15.4; DB 1; Length 3456;
Best Local Similarity 94.1%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CCTGCACAGCAGTCTTA 18
Db      65 CCTGCACAGCAGTCTTA 49

RESULT 11
US-09-780-172-18/c
Sequence 18, Application US/09780172
Patent No. 6607916
GENERAL INFORMATION:
APPLICANT: Robert McKay
APPLICANT: Susan M. Freier
APPLICANT: Jacqueline Wyatc
TITLE OF INVENTION: ANTISENSE MODULATION OF CASEIN KINASE 2-ALPHA EXPRESSION
FILE REFERENCE: RRS-0159
CURRENT APPLICATION NUMBER: US/09/780,172
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 96
SEQ ID NO 18
LENGTH: 63000
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
US-09-780-172-18

Query Match          77.0%; Score 15.4; DB 4; Length 63000;
Best Local Similarity 94.1%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CCTGCACAGCAGTCTTA 18
Db      56617 CCTGCACATCAGTCTTA 56601

RESULT 12
US-09-313-294A-5792/c
Sequence 5792, Application US/09313294A
Patent No. 6476212
GENERAL INFORMATION:
APPLICANT: Lalguadi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
SEQ ID NO 5792
LENGTH: 278
TYPE: DNA
ORGANISM: Zea mays
```

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FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6476212 700350690H1
NAME/KEY: unsure
LOCATION: 14, 17, 22-23, 55, 85, 151, 159, 181, 185, 202, 212, 229, 240, 245, 251,
OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-5792

Query Match          76.0%; Score 15.2; DB 4; Length 278;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 CCTGCACAGCAGTCTTAGG 20
Db      49 CGCTGCACGCAGGTTTAGG 30

RESULT 13
US-09-313-294A-987/c
Sequence 987, Application US/09313294A
Patent No. 6476212
GENERAL INFORMATION:
APPLICANT: Lalguadi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
SEQ ID NO 987
LENGTH: 286
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6476212 700550186H1
US-09-313-294A-987

Query Match          76.0%; Score 15.2; DB 4; Length 286;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 CCTGCACAGCAGTCTTAGG 20
Db      73 CGCTGCACGCAGGTTTAGG 54

RESULT 14
US-09-023-655-471/c
Sequence 471, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Sellhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREMITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 471:
SEQUENCE CHARACTERISTICS:
LENGTH: 328 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: COLN00708
CLONE: 1844277
US-09-023-655-471

Query Match 76.0%; Score 15.2; DB 4; Length 328;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCTGCACAGCAGTCTTAGG 20
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Db 116 CACTGCACAGCAGTCTGAGG 97

RESULT 15
US-09-733-167A-8/C
Sequence 8, Application US/09733167A
Patent No. 6696547
GENERAL INFORMATION:
APPLICANT: Peter, Marcus
TITLE OF INVENTION: Protein for Regulation of Apoptosis
FILE REFERENCE: 4121-120
CURRENT APPLICATION NUMBER: US/09/733,167A
CURRENT FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: PCT/DE99/01712
PRIOR FILING DATE: 1999-06-08
PRIOR APPLICATION NUMBER: German Patent Application No. 6696547 198 25 621.3
PRIOR FILING DATE: 1998-06-08
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patent version 3.1
SEQ ID NO 8
LENGTH: 630
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Truncated segment of the DNA sequence encoding human DBD, compri
OTHER INFORMATION: sing nucleotides 352-981 of SEQ ID NO 2.
US-09-733-167A-8

Query Match 76.0%; Score 15.2; DB 4; Length 630;
Best Local Similarity 85.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCTGCACAGCAGTCTTAGG 20
| | | | | | | | | | | | | | | | | | | | | |
Db 311 CCTGCACAGCAGTCTCATG 292

Search completed: January 26, 2005, 13:15:25
Job time : 30.4583 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 26, 2005, 13:15:32 ; Search time 141.778 Seconds
(without alignments)
810.549 Million cell updates/sec

Title: US-10-085-612A-22

Perfect score: 20
Sequence: 1 cccgcacagcagctttagg 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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20: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
C 1	20	100.0	1254 14 US-10-085-612-4	Sequence 4, Appl1
C 2	17.4	87.0	312 9 US-09-841-132-466	Sequence 466, App
C 3	17.4	87.0	312 18 US-10-872-155-466	Sequence 466, App
C 4	17.4	87.0	617 13 US-10-027-632-259078	Sequence 259078,
C 5	17.4	87.0	617 15 US-10-027-632-259078	Sequence 259078,
C 6	17.4	87.0	1230025 16 US-10-289-762-1	Sequence 1, Appl1
C 7	16.8	84.0	201 18 US-10-719-993-18096	Sequence 18096, A
C 8	16.8	84.0	201 18 US-10-719-993-47222	Sequence 47222, A
C 9	16.8	84.0	285 18 US-10-425-115-25647	Sequence 25647, A
C 10	16.8	84.0	488 9 US-09-864-761-11190	Sequence 11190, A
C 11	16.8	84.0	977 18 US-10-653-047-1353	Sequence 1353, Ap
C 12	16.8	84.0	1156 13 US-10-027-632-119142	Sequence 119142,

13	16.8	84.0	1156	15	US-10-027-632-119142	Sequence 119142,
14	16.8	84.0	2111	10	US-09-854-867-145	Sequence 145, App
15	16.8	84.0	2487	14	US-10-082-830-67	Sequence 67, Appl
16	16.8	84.0	2492	9	US-09-096-648-3	Sequence 3, Appl1
17	16.8	84.0	2492	9	US-09-799-462A-3	Sequence 3, Appl1
18	16.8	84.0	2492	10	US-09-836-911A-3	Sequence 3, Appl1
19	16.8	84.0	2492	13	US-10-125-767-3	Sequence 3, Appl1
20	16.8	84.0	2492	14	US-10-151-081-3	Sequence 3, Appl1
21	16.8	84.0	2492	15	US-10-287-113-3	Sequence 3, Appl1
22	16.8	84.0	2492	15	US-10-219-694-3	Sequence 3, Appl1
23	16.8	84.0	2492	17	US-10-782-129-3	Sequence 3, Appl1
24	16.8	84.0	2492	17	US-10-808-689-3	Sequence 3, Appl1
25	16.8	84.0	2517	15	US-10-281-673-5	Sequence 5, Appl1
26	16.8	84.0	52312	17	US-10-322-281-753	Sequence 753, App
27	16.8	84.0	152165	18	US-10-719-993-6942	Sequence 6942, Ap
C 28	16.8	84.0	1980090	18	US-10-719-993-6815	Sequence 6815, Ap
29	16.4	82.0	696	18	US-10-653-047-7191	Sequence 7191, Ap
30	16.4	82.0	1089	9	US-09-841-132-467	Sequence 467, App
31	16.4	82.0	1089	18	US-10-872-155-467	Sequence 467, App
32	16	80.0	403035	17	US-10-741-601-5729	Sequence 5729, Ap
C 33	15.8	79.0	91	9	US-09-864-761-25055	Sequence 25055, A
34	15.8	79.0	201	18	US-10-719-993-24938	Sequence 24938, A
35	15.8	79.0	241	15	US-10-029-386-22007	Sequence 22007, A
C 36	15.8	79.0	262	9	US-09-864-761-27307	Sequence 27307, A
C 37	15.8	79.0	457	9	US-09-864-761-10658	Sequence 10658, A
C 38	15.8	79.0	498	13	US-10-027-632-133950	Sequence 133950,
C 39	15.8	79.0	498	15	US-10-027-632-133950	Sequence 133950,
C 40	15.8	79.0	517	10	US-09-770-961-89	Sequence 89, Appl
C 41	15.8	79.0	519	9	US-09-864-761-8324	Sequence 8324, Ap
C 42	15.8	79.0	562	13	US-10-027-632-286546	Sequence 286546,
C 43	15.8	79.0	562	15	US-10-027-632-286546	Sequence 286546,
C 44	15.8	79.0	565	15	US-10-029-386-8307	Sequence 8307, Ap
C 45	15.8	79.0	660	13	US-10-027-632-135364	Sequence 135364,

ALIGNMENTS

RESULT 1
US-10-085-612-4/C
; Sequence 4, Application US/10085612
; Publication No. US20030096251A1
; GENERAL INFORMATION:
; APPLICANT: Guida, Marco
; APPLICANT: Hall, Jeff
; APPLICANT: Petros, William
; APPLICANT: Vredenburg, James
; APPLICANT: Colvin, Oliver
; APPLICANT: Marks, Jeffrey
; TITLE OF INVENTION: Methods for Evaluating the Ability to Metabolize Pharmaceuticals
; FILE REFERENCE: 4389-5-C1
; CURRENT APPLICATION NUMBER: US/10/085,612
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/144,367
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/271,630
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 1254
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-085-612-4

Query Match 100.0%; Score 20; DB 14; Length 1254;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 20; Conservative 0; Mismatches 0; Gaps 0;
Db 1094 CCTGCACAGCAGCTTtagg 1075
1 CCTGCACAGCAGCTTtagg 20
|||||
|||

RESULT 2
US-09-841-132-466/c
; Sequence 466, Application US/09841132
; Patent No. US20020061848A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOSITIONS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C8
; CURRENT APPLICATION NUMBER: US/09/841.132
; CURRENT FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 466
; LENGTH: 312
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-841-132-466

Query Match 87.0%; Score 17.4; DB 9; Length 312;
Best Local Similarity 94.7%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 CCTGCACAGCAGCTTAGG 20
Db 253 CCTGCAAGCAGCTTAGG 235

RESULT 3
US-10-872-155-466/c
; Sequence 466, Application US/10872155
; Publication No. US20040234536A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C10
; CURRENT APPLICATION NUMBER: US/10/872.155
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 09/620,412
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 09/598,419
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: 09/556,877
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: 09/454,684
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 09/426,571
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 09/410,568
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 09/288,594
; PRIOR FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: 09/208,277
; PRIOR FILING DATE: 1998-12-08
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 466
; LENGTH: 312
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-872-155-466

Query Match 87.0%; Score 17.4; DB 18; Length 312;
Best Local Similarity 94.7%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 CCTGCACAGCAGCTTAGG 20
Db 253 CCTGCAAGCAGCTTAGG 235

RESULT 4
US-10-027-632-259078/c
; Sequence 259078, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 259078
; LENGTH: 617
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-259078

Query Match 87.0%; Score 17.4; DB 13; Length 617;
Best Local Similarity 94.7%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCTGCACAGCAGCTTAGG 19
Db 239 CCTGCACAGCAATCTTAG 221

RESULT 5
US-10-027-632-259078/c
; Sequence 259078, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720

```
SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 259078
; LENGTH: 617
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-259078

Query Match      87.0%; Score 17.4; DB 15; Length 617;
Best Local Similarity 94.7%; Pred. No. 39;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CCCTGCACAGCAGCTCTTAG 19
        |||||
Db      239 CCCTGCACAGCAATCTTAG 221

RESULT 6
US-10-289-762-1/c
; Sequence 1, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Grifflars, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1
; LENGTH: 1230025
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(15000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15001)..(30000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (30001)..(45000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (45001)..(60000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (60001)..(75000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (75001)..(90000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (90001)..(105000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (105001)..(120000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (120001)..(135000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (135001)..(150000)
; OTHER INFORMATION: n=a or c or g or t
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FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (150001)..(165000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (165001)..(180000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (180001)..(195000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (195001)..(210000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (210001)..(225000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (225001)..(240000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (240001)..(255000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (255001)..(270000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (270001)..(285000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (285001)..(300000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (300001)..(315000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (315001)..(330000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (330001)..(345000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (345001)..(360000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (360001)..(375000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (375001)..(390000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (390001)..(405000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (405001)..(420000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
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NAME/KEY: misc_feature
LOCATION: (42001)..(435000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (43501)..(450000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (45001)..(465000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (46501)..(480000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (48001)..(495000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (49501)..(510000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (51001)..(525000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (52501)..(540000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (54001)..(555000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (55501)..(570000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (57001)..(585000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (58501)..(600000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (60001)..(615000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (61501)..(630000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (63001)..(645000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (64501)..(660000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (66001)..(675000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (67501)..(690000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
```

```
Query Match 87.0%; Score 17.4; DB 16; Length 1230025;
Best Local Similarity 94.7%; Pred. No. 42;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 CCTGCACAGCAGCTTTAGG 20
Db 691511 CTTCCAAAGCAGCTTTAGG 691493
```

```
RESULT 7
US-10-719-993-18096/c
Sequence 18096, Application US/10719993
Publication No. US20040265849A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
FILE REFERENCE: CU001496
CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 55342
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 18096
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-10-719-993-18096
```

```
Query Match 84.0%; Score 16.8; DB 18; Length 201;
Best Local Similarity 90.0%; Pred. No. 79;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 1 CCTGCACAGCAGCTTTAGG 20
Db 126 CCATACACAGCAGCTTTAGG 107
```

```
RESULT 8
US-10-719-993-47222
Sequence 47222, Application US/10719993
Publication No. US20040265849A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
FILE REFERENCE: CU001496
CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 55342
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 47222
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-10-719-993-47222
```

```
Query Match 84.0%; Score 16.8; DB 18; Length 201;
Best Local Similarity 90.0%; Pred. No. 79;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 1 CCTGCACAGCAGCTTTAGG 20
Db 76 CCATACACAGCAGCTTTAGG 95
```

```
RESULT 9
US-10-425-115-25647
Sequence 25647, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
```


APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 25647
LENGTH: 285
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_1233C.1
US-10-425-115-25647

Query Match 84.0%; Score 16.8; DB 18; Length 285;
Best Local Similarity 90.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTGCACAGCAGCTTTAGG 20
DB 222 CCATGCACAGCAGCTTTATG 241

RESULT 10
US-09-864-761-11190
Sequence 11190, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecm1ca-X-1
CURRENT FILING DATE: 2001-05-23
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203

PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 11190
LENGTH: 488
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC005879.2
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.82
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.7
OTHER INFORMATION: EXPRESSED IN LONG, SIGNAL = 0.88
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.68
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.62
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.72
US-09-864-761-11190

Query Match 84.0%; Score 16.8; DB 9; Length 488;
Best Local Similarity 90.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTGCACAGCAGCTTTAGG 20
DB 242 CCTGCACAGCAGCCTTAGG 261

RESULT 11
US-10-653-047-1353
Sequence 1353, Application US/10653047
Publication No. US20040229367A1
GENERAL INFORMATION:
APPLICANT: Randy M. Berka
APPLICANT: Michael W. Ray
APPLICANT: Jeffrey R. Shuster
APPLICANT: Sakari Kauppinen
APPLICANT: Ib Groth Clausen
APPLICANT: Peter Bjarke Olsen
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
FILE REFERENCE: 5849.200-US
CURRENT APPLICATION NUMBER: US/10/653,047
CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US/09/533,559
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/273,623
PRIOR FILING DATE: 1999-03-22
NUMBER OF SEQ ID NOS: 7860
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1353
LENGTH: 977
TYPE: DNA
ORGANISM: Fusarium venenatum
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)---(977)
OTHER INFORMATION: n = A,T,C or G
US-10-653-047-1353

Query Match 84.0%; Score 16.8; DB 18; Length 977;
Best Local Similarity 90.0%; Pred. No. 81;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTGCACAGCAGCTTTAGG 20
DB 192 CCTGCACAGCAGCTCAGG 211

RESULT 12
US-10-027-632-119142
Sequence 119142, Application US/10027632
Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.

```
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 119142
; LENGTH: 1156
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-119142
```

```
Query Match      84.0%; Score 16.8; DB 13; Length 1156;
Best Local Similarity 90.0%; Pred. No. 81;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1  CCTGCACAGCAGCTTTAGG 20
          |||||
Db      693  CCTGCACAGCAGCTTTGGG 712
```

```
RESULT 13
US-10-027-632-119142
; Sequence 119142, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 119142
; LENGTH: 1156
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-119142
```

```
Query Match      84.0%; Score 16.8; DB 15; Length 1156;
Best Local Similarity 90.0%; Pred. No. 81;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1  CCTGCACAGCAGCTTTAGG 20
          |||||
Db      693  CCTGCACAGCAGCTTTGGG 712

RESULT 14
US-09-854-867-145
; Sequence 145, Application US/09854867
; Publication No. US20030224356A1
; GENERAL INFORMATION:
; APPLICANT: JOAN, KNOEL, H
; APPLICANT: ROGAN, PETER K
; TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING
; FILE REFERENCE: 30307
; CURRENT APPLICATION NUMBER: US/09/854,867
; CURRENT FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 613
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 145
; LENGTH: 2111
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: (1)..(2111)
; OTHER INFORMATION: ta11
US-09-854-867-145
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```
Query Match      84.0%; Score 16.8; DB 10; Length 2111;
Best Local Similarity 90.0%; Pred. No. 81;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1  CCTGCACAGCAGCTTTAGG 20
          |||||
Db      133  CCTGCACAGCAGCTTTAGG 152
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```
RESULT 15
US-10-082-830-67
; Sequence 67, Application US/10082830
; Publication No. US2003007604A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Yongming
; APPLICANT: Recipon, Herve
; APPLICANT: Salceda, Susana
; APPLICANT: Liu, Chenghua
; APPLICANT: Turner, Leah
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific
; FILE REFERENCE: DEX-0249
; CURRENT APPLICATION NUMBER: US/10/082,830
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,802
; PRIOR FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 282
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
; LENGTH: 2487
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-082-830-67
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Query Match      84.0%; Score 16.8; DB 14; Length 2487;
Best Local Similarity 90.0%; Pred. No. 81;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY      1  CCTGCACAGCAGCTTTAGG 20
          |||||
Db      977  CCTGCACAGCAGCTTTAGG 996
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Search completed: January 26, 2005, 18:15:51
Job time : 144.778 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 26, 2005, 11:30:01 ; Search time 30.0667 Seconds
(without alignments)
520.089 Million cell updates/sec

Title: US-10-085-612A-23

Perfect score: 22

Sequence: 1 ctgcagcccccaccctctccccc 22

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PTUS.COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17.8	80.9	452	4	US-09-322-357-47
2	17.8	80.9	867	4	US-09-270-767-12497
3	17.4	79.1	795	4	US-09-795-926-47
4	17.4	79.1	1505	1	US-07-915-246-1
5	17.4	79.1	4638	4	US-09-023-655-1215
6	17.2	78.2	284	4	US-09-313-294A-6532
7	17.2	78.2	309	1	US-08-209-747-3
8	17.2	78.2	309	1	US-08-458-298-3
9	17.2	78.2	451	4	US-09-702-705-1647
10	17.2	78.2	451	4	US-09-736-457-1647
11	17.2	78.2	451	4	US-09-614-124B-1647
12	17.2	78.2	451	4	US-09-671-325-1647
13	17.2	78.2	451	4	US-09-658-824-1647
14	17.2	78.2	492	4	US-09-621-976-1517
15	17.2	78.2	543	4	US-09-621-976-1516
16	17.2	78.2	557	4	US-10-101-464A-168
17	17.2	78.2	1129	3	US-09-387-699-1
18	17.2	78.2	1129	3	US-09-641-259B-1
19	17.2	78.2	1200	4	US-09-598-401C-36
20	17.2	78.2	1407	3	US-08-688-988-7
21	17.2	78.2	2793	1	US-07-646-537B-1
22	17.2	78.2	2933	3	US-08-999-774A-5
23	17.2	78.2	2933	4	US-09-149-476-165
24	17.2	78.2	2995	4	US-09-244-805-26
25	17.2	78.2	3028	4	US-09-392-714-2
26	17.2	78.2	3246	4	US-09-270-767-13706
27	17.2	78.2	3276	4	US-09-149-476-298

C 28	17.2	78.2	3768	4	US-09-566-921-50	Sequence 50, Appl
C 29	17.2	78.2	3812	4	US-09-784-316-1	Sequence 1, Appl
C 30	17.2	78.2	3812	4	US-10-229-124-1	Sequence 1, Appl
C 31	17.2	78.2	6775	4	US-09-620-312D-289	Sequence 289, App
C 32	17.2	78.2	7672	4	US-09-220-132-24	Sequence 24, Appl
C 33	17.2	78.2	8091	4	US-09-230-652-1	Sequence 1, Appl
C 34	17.2	78.2	8257	4	US-09-484-970B-65	Sequence 65, Appl
C 35	17.2	78.2	19025	4	US-09-849-334-3	Sequence 3, Appl
C 36	17.2	78.2	19025	4	US-10-274-878-3	Sequence 3, Appl
C 37	17.2	78.2	65042	4	US-09-784-316-3	Sequence 3, Appl
C 38	17.2	78.2	65042	4	US-10-229-124-3	Sequence 3, Appl
C 39	17	77.3	206	4	US-09-621-976-9654	Sequence 9654, Ap
C 40	17	77.3	311	4	US-09-621-976-11167	Sequence 11167, A
C 41	17	77.3	447	4	US-09-621-976-14007	Sequence 14007, A
C 42	17	77.3	458	4	US-09-621-976-12510	Sequence 12510, A
C 43	17	77.3	477	4	US-09-621-976-12572	Sequence 12572, A
C 44	17	77.3	480	4	US-09-621-976-10666	Sequence 10666, A
C 45	17	77.3	481	4	US-09-621-976-10533	Sequence 10533, A

ALIGNMENTS

RESULT 1
US-09-322-357-47
Sequence 47, Application US/09322357

Patent No. 6593104

GENERAL INFORMATION:

APPLICANT: STONE, EDWIN M.

FILE REFERENCE: SHEFFIELD, VAL C.

TITLE OF INVENTION: MACULAR DEGENERATION DIAGNOSTICS AND THERAPEUTICS

CURRENT FILING DATE: 1999-05-28

CURRENT FILING DATE: 1999-05-28

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 47

LENGTH: 452

TYPE: DNA

ORGANISM: Homo sapiens

US-09-322-357-47

Query Match
Best Local Similarity 90.5%; Score 17.8; DB 4; Length 452;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGCAGCCCACTCTCTCC 22
Db 45 TGCAGCCCACTCTCTCC 65

RESULT 2

US-09-270-767-12497/c
Sequence 12497, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REFERENCE: File Reference: 7326-094

CURRENT FILING DATE: 1999-03-17

CURRENT FILING DATE: 1999-03-17

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 12497

LENGTH: 867

TYPE: DNA

ORGANISM: Drosophila melanogaster

US-09-270-767-12497

Query Match
Best Local Similarity 90.5%; Score 17.8; DB 4; Length 867;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGCAGCCCACTCTCTCC 22
Db 463 TGCAGCCCACTCTCTCC 443

RESULT 3

US-09-926-47/c
Sequence 47, Application US/09795926
Patent No. 6555669
GENERAL INFORMATION:
APPLICANT: Donoho, Gregory
APPLICANT: Hilbun, Erin
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Friedlich, Glenn
APPLICANT: Abuin, Alejandro
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
APPLICANT: Walke, D. Wade
APPLICANT: Wilanowski, Nathaniel L.
APPLICANT: Hu, Yi
APPLICANT: Kieke, James Alvin
APPLICANT: Potter, David George
TITLE OF INVENTION: NOVEL HUMAN TRANSFERASE PROTEINS AND
FILE REFERENCE: LEX-0144-USA
CURRENT APPLICATION NUMBER: US/09/795,926
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 60/185,920
PRIOR FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: US 60/186,558
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 60/191,849
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 47
LENGTH: 795
TYPE: DNA
ORGANISM: homo sapiens
US-09-795-926-47

Query March 79.1%; Score 17.4; DB 4; Length 795;
Best Local Similarity 94.7%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCCCACTCTCTCC 22
Db 123 CAGCCCACTCTCTCC 105

RESULT 4

US-07-915-246-1/c
Sequence 1, Application US/07915246
Patent No. 5401836
GENERAL INFORMATION:
APPLICANT: Baszczynski, Chris L.
APPLICANT: Fallis, Lynne
APPLICANT: Bellmare, Guy
APPLICANT: Boivin, Rodolphe
TITLE OF INVENTION: A BRASSICA REGULATORY SEQUENCE FOR
TITLE OF INVENTION: ROOT-SPECIFIC OR ROOT-ABUNDANT GENE EXPRESSION
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held, and Malloy
STREET: 500 W. Madison St. 34th Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/915,246
FILING DATE: 19920716
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pochopien, Donald J.
REGISTRATION NUMBER: 32,167
REFERENCE/DOCKET NUMBER: 91 P 1125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312 707-8869
TELEFAX: 312 707-9155
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1505 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Brassica napus
STRAIN: Westar
DEVELOPMENTAL STAGE: Somatic
TISSUE TYPE: Root
US-07-915-246-1

Query March 79.1%; Score 17.4; DB 1; Length 1505;
Best Local Similarity 94.7%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCCCACTCTCTCC 22
Db 756 CAGCCCACTCTCTCC 738

RESULT 5

US-09-023-655-1215/c
Sequence 1215, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Sellhammer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:

```

RESULT 7
US-08-209-747-3/c
: Sequence 3, Application US/08209747
: Patent No. 5733771
:
: GENERAL INFORMATION:
:
: APPLICANT: Lewis, Randolph V.
: APPLICANT: Colgalt, Mark
: TITLE OF INVENTION: cDNAs Encoding Minor Ampullate Spider
: TITLE OF INVENTION: Silk Proteins
: NUMBER OF SEQUENCES: 56
:
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Birch, Stewart, Kolaesch & Birch
: STREET: P. O. Box 747
: CITY: Falls Church
: STATE: Virginia
: COUNTRY: USA
: ZIP: 22040-3487
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk

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RESULT 8
 US-08-458-298-3/c
 Sequence 3, Application US/08458298
 Patent No. 5756677
 GENERAL INFORMATION:
 APPLICANT: Lewis, Randolph V.
 APPLICANT: Colgin, Mark
 TITLE OF INVENTION: CDNA Encoding Minor Ampullate Spider
 TITLE OF INVENTION: Silk Proteins
 NUMBER OF SEQUENCES: 56
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Birch, Stewart, Kolasch & Birch
 STREET: P.O. Box 747
 CITY: Falls Church
 STATE: Virginia
 COUNTRY: USA
 ZIP: 22040-3487
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/458,298
 FILING DATE: 02-JUN-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/209,747
 FILING DATE: 14-MAR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Murphy Jr., Gerald M.
 REGISTRATION NUMBER: 28,977

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REFERENCE/DOCKET NUMBER: 1447-104P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: N. clavipes
TISSUE TYPE: minor ampullate gland
FEATURE:
NAME/KEY: CDS
LOCATION: 1..309
OTHER INFORMATION: /product= "amino terminus of MISF2
US-08-458-298-3
OTHER INFORMATION: protein"
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Query Match 78.2%; Score 17.2; DB 1; Length 309;
Best Local Similarity 86.4%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 1 CTGCAGCCGCCACCTCTTCTCC 22
Db 307 CTGCAGCCGCCACCTCTTCTCC 286
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RESULT 9
US-09-702-705-1647
Sequence 1647, Application US/09702705
Patent No. 6504010
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darriack
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.478C14
CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 1833
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1647
LENGTH: 451
TYPE: DNA
ORGANISM: Homo sapiens
US-09-702-705-1647
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Query Match 78.2%; Score 17.2; DB 4; Length 451;
Best Local Similarity 86.4%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 1 CTGCAGCCGCCACCTCTTCTCC 22
Db 301 CAGCAGCCGCCACCATCTCC 322
```

```
RESULT 10
US-09-736-457-1647
Sequence 1647, Application US/09736457
Patent No. 6509448
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
```

```
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darriack
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.478C15
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1647
LENGTH: 451
TYPE: DNA
ORGANISM: Homo sapiens
US-09-736-457-1647
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Query Match 78.2%; Score 17.2; DB 4; Length 451;
Best Local Similarity 86.4%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 1 CTGCAGCCGCCACCTCTTCTCC 22
Db 301 CAGCAGCCGCCACCATCTCC 322
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RESULT 11
US-09-614-124B-1647
Sequence 1647, Application US/09614124B
Patent No. 6630574
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darriack
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.478C9
CURRENT APPLICATION NUMBER: US/09/614,124B
CURRENT FILING DATE: 2001-07-11
NUMBER OF SEQ ID NOS: 1668
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1647
LENGTH: 451
TYPE: DNA
ORGANISM: Homo sapiens
US-09-614-124B-1647
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Query Match 78.2%; Score 17.2; DB 4; Length 451;
Best Local Similarity 86.4%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 1 CTGCAGCCGCCACCTCTTCTCC 22
Db 301 CAGCAGCCGCCACCATCTCC 322
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RESULT 12
US-09-671-325-1647
Sequence 1647, Application US/09671325
Patent No. 6667154
GENERAL INFORMATION:
APPLICANT: Bangur, Chaitanya S.
```


APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvik, Tom
APPLICANT: Carter, Derrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.478C12
CURRENT APPLICATION NUMBER: US/09/671,325
CURRENT FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 1825
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1647.
LENGTH: 451
TYPE: DNA
ORGANISM: Homo sapiens
US-09-671-325-1647

Query Match 78.2% Score 17.2; DB 4; Length 451;
Best Local Similarity 86.4%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTGCAGCCGCCACCTCTTCTCC 22
Db 301 CAGCAGCCGCCACCATCTCC 322

RESULT 13
US-09-658-824-1647
Sequence 1647, Application US/09658824
Patent No. 6746846
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaltanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvik, Tom
APPLICANT: Carter, Derrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.478C11
CURRENT APPLICATION NUMBER: US/09/658,824
CURRENT FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 1788
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1647
LENGTH: 451
TYPE: DNA
ORGANISM: Homo sapiens
US-09-658-824-1647

Query Match 78.2% Score 17.2; DB 4; Length 451;
Best Local Similarity 86.4%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTGCAGCCGCCACCTCTTCTCC 22
Db 301 CAGCAGCCGCCACCATCTCC 322

RESULT 14
US-09-621-976-107
Sequence 107, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent .pm
SEQ ID NO 107
LENGTH: 492
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 257..490
NAME/KEY: sig.peptide
LOCATION: 257..325
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 6.6999980926514
OTHER INFORMATION: seq LCPSICMCSVSLA/CV
US-09-621-976-107

Query Match 78.2% Score 17.2; DB 4; Length 492;
Best Local Similarity 86.4%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTGCAGCCGCCACCTCTTCTCC 22
Db 23 CTGCAGCCGCCACCTCTTCTCC 44

RESULT 15
US-09-621-976-1516
Sequence 1516, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent .pm
SEQ ID NO 1516
LENGTH: 543
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 257..505
NAME/KEY: sig.peptide
LOCATION: 257..325
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 6.6999980926514
OTHER INFORMATION: seq LCPSICMCSVSLA/CV
US-09-621-976-1516

Query Match 78.2% Score 17.2; DB 4; Length 543;
Best Local Similarity 86.4%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTGCAGCCGCCACCTCTTCTCC 22
Db 23 CTGCAGCCGCCACCTCTTCTCC 44

Search completed: January 26, 2005, 13:15:26
Job time : 31.1917 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 26, 2005, 13:15:32 ; Search time 155.956 Seconds
(without alignments)
810.549 Million cell updates/sec

Title: US-10-085-612A-23

Perfect score: 22

Sequence: 1 ctcgagcccccactctctcc 22

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues 8600550

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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19: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:*
20: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq:*
21: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	1254	14	US-10-085-612-4
2	20.4	92.7	29560	17	US-10-322-281-791
3	18.8	85.5	1188	15	US-10-369-493-31701
4	18.8	85.5	1599	16	US-10-425-114-22378
5	18.8	85.5	2076	18	US-10-739-930-4643
6	18.8	85.5	2149	17	US-10-767-701-9631
7	18.8	85.5	2765	16	US-10-108-260A-2264
8	18.8	85.5	3096	15	US-10-295-027-775
9	18.8	85.5	3096	15	US-10-295-027-792
10	18.8	85.5	3096	15	US-10-295-027-819
11	18.8	85.5	3096	15	US-10-295-027-894
12	18.8	85.5	37252	13	US-10-087-192-1228

C 13	18.8	85.5	235070	13	US-10-087-192-1990	Sequence 1990, Ap
C 14	18.4	83.6	1164	15	US-10-369-493-43210	Sequence 43210, A
C 15	17.8	80.9	201	17	US-10-741-601-1452	Sequence 1452, Ap
C 16	17.8	80.9	201	17	US-10-741-601-1495	Sequence 1495, Ap
C 17	17.8	80.9	251	18	US-10-425-115-8310	Sequence 8310, A
C 18	17.8	80.9	278	9	US-09-923-876-3761	Sequence 3761, Ap
C 19	17.8	80.9	429	9	US-09-864-761-2884	Sequence 2884, Ap
C 20	17.8	80.9	506	17	US-10-767-701-17455	Sequence 17455, A
C 21	17.8	80.9	821	17	US-10-437-963-10139	Sequence 10139, A
C 22	17.8	80.9	821	17	US-10-437-963-10139	Sequence 162309, A
C 23	17.8	80.9	887	18	US-10-425-115-162309	Sequence 2385, Ap
C 24	17.8	80.9	1907	16	US-10-425-114-2385	Sequence 53593, A
C 25	17.8	80.9	1960	13	US-10-027-632-53593	Sequence 53593, A
C 26	17.8	80.9	1960	15	US-10-027-632-53593	Sequence 174824, A
C 27	17.8	80.9	2041	18	US-10-425-115-174824	Sequence 14264, A
C 28	17.8	80.9	2124	17	US-10-437-963-14264	Sequence 114681, A
C 29	17.8	80.9	3018	15	US-10-027-632-114681	Sequence 114681, A
C 30	17.8	80.9	3018	15	US-10-027-632-114681	Sequence 30, Appl
C 31	17.8	80.9	13635	16	US-10-464-368-30	Sequence 671, App
C 32	17.8	80.9	13635	16	US-10-210-175-13	Sequence 671, App
C 33	17.8	80.9	13836	13	US-10-087-192-671	Sequence 356, App
C 34	17.8	80.9	14887	16	US-10-276-774-372	Sequence 372, App
C 35	17.8	80.9	14889	15	US-10-101-510-356	Sequence 356, App
C 36	17.8	80.9	14896	11	US-09-750-972-6	Sequence 206, App
C 37	17.8	80.9	14896	16	US-10-159-563-206	Sequence 243, App
C 38	17.8	80.9	14896	18	US-10-473-974-243	Sequence 154, App
C 39	17.8	80.9	32874	16	US-10-052-482-154	Sequence 670, App
C 40	17.8	80.9	104083	13	US-10-087-192-670	Sequence 1456, Ap
C 41	17.4	79.1	201	17	US-10-741-601-1456	Sequence 1500, Ap
C 42	17.4	79.1	201	17	US-10-741-601-1500	Sequence 10243, A
C 43	17.4	79.1	201	17	US-10-741-601-10243	Sequence 31051, A
C 44	17.4	79.1	497	17	US-10-767-701-31051	Sequence 26731, A
C 45	17.4	79.1	541	17	US-10-767-701-26731	

ALIGNMENTS

RESULT 1

US-10-085-612-4

Sequence 4, Application US/10085612

Publication No. US20030096251A1

GENERAL INFORMATION:

APPLICANT: Guida, Marco

APPLICANT: Hall, Jeff

APPLICANT: Petros, William

APPLICANT: Vredenburg, James

APPLICANT: Colvin, Oliver

APPLICANT: Marks, Jeffrey

TITLE OF INVENTION: Methods for Evaluating the Ability to Metabolize Pharmaceuticals

FILE REFERENCE: 4389-5-C1

CURRENT APPLICATION NUMBER: US/10/085,612

CURRENT FILING DATE: 2002-02-26

PRIOR APPLICATION NUMBER: 09/144,367

PRIOR FILING DATE: 1998-08-31

PRIOR APPLICATION NUMBER: 60/271,630

PRIOR FILING DATE: 2001-02-26

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PatentIn version 3.0

SEQ ID NO 4

LENGTH: 1254

TYPE: DNA

ORGANISM: Homo sapiens

US-10-085-612-4

Query Match 100.0%; Score 22; DB 14; Length 1254;

Best Local Similarity 100.0%; Pred. No. 9.5;

Matches 22; Conservative 0; Mismatches 0; Gaps 0;

DB 1027 CTCGAGCCCACTCTCTCC 1048

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RESULT 2
US-10-322-281-791
; Sequence 791, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 791
; LENGTH: 29560
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1) ... (29560)
; OTHER INFORMATION: n = A,T,C or G
US-10-322-281-791

Query Match          92.7%; Score 20.4; DB 17; Length 29560;
Best Local Similarity 95.5%; Pred. No. 27;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGAGGCCCCACCTCTCTCTCC 22
Db 23106 CAGCAGCCCCACCTCTCTCTCC 23127

RESULT 3
US-10-369-493-31701/C
; Sequence 31701, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 31701
; LENGTH: 1188
; TYPE: DNA
; ORGANISM: Rhodobacter sphaeroides
US-10-369-493-31701

Query Match          85.5%; Score 18.8; DB 15; Length 1188;
Best Local Similarity 90.9%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGAGGCCCCACCTCTCTCTCC 22
Db 1056 CTGAGGCCCCACCTCTCTCTCC 1035

RESULT 4
US-10-425-114-22378
; Sequence 22378, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua
APPLICANT: Kovacic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 22378
LENGTH: 1599
TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: LIB3478-020-C3_FLI
US-10-425-114-22378

Query Match          85.5%; Score 18.8; DB 16; Length 1599;
Best Local Similarity 90.9%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGAGGCCCCACCTCTCTCTCC 22
Db 864 CCGAGCAGCACCACCTCTCTCTCC 885

RESULT 5
US-10-739-930-4643/C
; Sequence 4643, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovacic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 4643
; LENGTH: 2076
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; OTHER INFORMATION: Clone ID: TRIAE-23APR03-CLUSTER29141_1
US-10-739-930-4643

Query Match          85.5%; Score 18.8; DB 18; Length 2076;
Best Local Similarity 90.9%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGAGGCCCCACCTCTCTCTCC 22
Db 253 CTGAGGCCCCACCTCTCTCTCC 232

RESULT 6
US-10-767-701-9631
; Sequence 9631, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 9631
; LENGTH: 2149
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; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAV03-CLUS27_1
US-10-767-701-9631

Query Match      85.5%; Score 18.8; DB 17; Length 2149;
Best Local Similarity 90.9%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CTGCAGCCCACTCTCTTCTCC 22
Db      1414 CCGCAGCAGCACCTCTCTTCTCC 1435

RESULT 7
US-10-108-260A-2264/c
; Sequence 2264, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2264
; LENGTH: 2765
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-108-260A-2264

Query Match      85.5%; Score 18.8; DB 16; Length 2765;
Best Local Similarity 90.9%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CTGCAGCCCACTCTCTTCTCC 22
Db      893 CTGCAGCCCACTCTCTTCTCC 872

RESULT 8
US-10-295-027-775/c
; Sequence 775, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezl, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
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; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 775
; LENGTH: 3096
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-295-027-775

Query Match      85.5%; Score 18.8; DB 15; Length 3096;
Best Local Similarity 90.9%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CTGCAGCCCACTCTCTTCTCC 22
Db      105 CTGCAGCAGCACCTCTCTTCTCC 84

RESULT 9
US-10-295-027-792/c
; Sequence 792, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezl, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 792
; LENGTH: 3096
; TYPE: DNA
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; ORGANISM: Homo sapiens
; US-10-295-027-792

Query Match      85.5%; Score 18.8; DB 15; Length 3096;
Best Local Similarity 90.9%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CTGCAGCCCCACCTCTCTTCTCC 22
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Db      105 CTGCAGCAGCACCTCTCTTCTCC 84

RESULT 10
US-10-295-027-819/c
; Sequence 819, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevez, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT FILING DATE: 2002-11-13
; PRIOR FILING DATE: 2002-11-13
; PRIOR FILING DATE: 2000-09-15
; PRIOR FILING DATE: 2000-09-15
; PRIOR FILING DATE: 2001-11-13
; PRIOR FILING DATE: 2001-11-15
; PRIOR FILING DATE: 2001-11-15
; PRIOR FILING DATE: 2001-11-15
; PRIOR FILING DATE: 2001-11-21
; PRIOR FILING DATE: 2001-11-21
; PRIOR FILING DATE: 2001-11-29
; PRIOR FILING DATE: 2001-11-29
; PRIOR FILING DATE: 2001-12-14
; PRIOR FILING DATE: 2001-12-14
; PRIOR FILING DATE: 2002-01-08
; PRIOR FILING DATE: 2002-01-08
; PRIOR FILING DATE: 2002-01-10
; PRIOR FILING DATE: 2002-02-08
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 819
; LENGTH: 3096
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-295-027-819

Query Match      85.5%; Score 18.8; DB 15; Length 3096;
Best Local Similarity 90.9%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CTGCAGCCCCACCTCTCTTCTCC 22
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Db      105 CTGCAGCAGCACCTCTCTTCTCC 84

RESULT 11
US-10-295-027-894/c
; Sequence 894, Application US/10295027
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; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevez, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT FILING DATE: 2002-11-13
; PRIOR FILING DATE: 2002-11-13
; PRIOR FILING DATE: 2000-09-15
; PRIOR FILING DATE: 2000-09-15
; PRIOR FILING DATE: 2001-11-13
; PRIOR FILING DATE: 2001-11-13
; PRIOR FILING DATE: 2001-11-15
; PRIOR FILING DATE: 2001-11-15
; PRIOR FILING DATE: 2001-11-21
; PRIOR FILING DATE: 2001-11-21
; PRIOR FILING DATE: 2001-11-29
; PRIOR FILING DATE: 2001-11-29
; PRIOR FILING DATE: 2001-12-14
; PRIOR FILING DATE: 2001-12-14
; PRIOR FILING DATE: 2002-01-08
; PRIOR FILING DATE: 2002-01-08
; PRIOR FILING DATE: 2002-01-10
; PRIOR FILING DATE: 2002-01-10
; PRIOR FILING DATE: 2002-02-08
; PRIOR FILING DATE: 2002-02-08
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 894
; LENGTH: 3096
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-295-027-894

Query Match      85.5%; Score 18.8; DB 15; Length 3096;
Best Local Similarity 90.9%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CTGCAGCCCCACCTCTCTTCTCC 22
      ||||| ||||| ||||| |||||
Db      105 CTGCAGCAGCACCTCTCTTCTCC 84

RESULT 12
US-10-087-192-1228/c
; Sequence 1228, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT FILING DATE: 2002-03-01
; PRIOR FILING DATE: 2002-03-01
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
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SEQ ID NO 1228
LENGTH: 37252
TYPE: DNA
ORGANISM: Homo sapiens
US-10-087-192-1228

Query Match 85.5%; Score 18.8; DB 13; Length 37252;
Best Local Similarity 90.9%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGAGCCCACTCTCTTCC 22
DB 36114 CTCCTGCCCACTCTTCC 36093

RESULT 13
US-10-087-192-1990/C
Sequence 1990, Application US/10087192
Publication No. US20020182586A1
GENERAL INFORMATION:
APPLICANT: Morris, David W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
FILE REFERENCE: 529452000122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1990
LENGTH: 235070
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(235070)
OTHER INFORMATION: n = A,T,C or G
US-10-087-192-1990

Query Match 85.5%; Score 18.8; DB 13; Length 235070;
Best Local Similarity 90.9%; Pred. No. 88;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGAGCCCACTCTTCTCC 22
DB 205859 CTGAGCCCACTCTTCTCC 205838

RESULT 14
US-10-369-493-43210/C
Sequence 43210, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfang
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 43210
LENGTH: 1164
TYPE: DNA

ORGANISM: Myxococcus xanthus
US-10-369-493-43210

Query Match 83.6%; Score 18.4; DB 15; Length 1164;
Best Local Similarity 95.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCAGCCCACTCTTCTCC 22
DB 988 GCAGCCCACTCTTCTCC 969

RESULT 15
US-10-741-601-1452
Sequence 1452, Application US/10741601
Publication No. US20040166519A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
FILE REFERENCE: CI001500
CURRENT APPLICATION NUMBER: US/10/741,601
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 26415
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1452
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-10-741-601-1452

Query Match 80.9%; Score 17.8; DB 17; Length 201;
Best Local Similarity 90.5%; Pred. No. 6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGCAGCCCACTCTTCTCC 22
DB 159 TGCAGCCCACTCTTCTCC 179

Search completed: January 26, 2005, 18:15:53
Job time : 157.956 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 26, 2005, 11:30:01 : Search time 28.7 Seconds
(without alignments)
520.089 Million cell updates/sec

Title: US-10-085-612A-24

Sequence: 1 ctgcagcccccgcctctctc 21

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
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6: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
1	17.8	84.8	1345	US-09-372-339-1	Sequence 1, Appl1
2	17.8	84.8	1345	US-09-372-339-2	Sequence 2, Appl1
3	17.8	84.8	1345	US-09-144-357-3	Sequence 3, Appl1
4	17.4	82.9	3545	US-08-480-474-10	Sequence 10, Appl1
5	16.8	80.0	189	US-09-270-767-29245	Sequence 29245, A
6	16.8	80.0	743	US-09-270-767-13305	Sequence 13305, A
7	16.8	80.0	2464	US-07-863-169A-4	Sequence 4, Appl1
8	16.8	80.0	2464	US-08-429-964-4	Sequence 4, Appl1
9	16.8	80.0	2464	US-07-935-087-4	Sequence 4, Appl1
10	16.8	80.0	2464	PCT-US93-08062-4	Sequence 4, Appl1
11	16.8	80.0	5574	US-09-917-254-40	Sequence 40, Appl1
12	16.8	80.0	7453	US-09-620-312D-248	Sequence 248, App
13	16.8	80.0	7501	US-09-620-312D-249	Sequence 249, App
14	16.8	80.0	7596	US-09-023-655-1463	Sequence 1463, App
15	16.8	80.0	31571	US-08-323-443B-1	Sequence 1, Appl1
16	16.8	80.0	53527	US-08-658-136-2	Sequence 2, Appl1
17	16.8	80.0	53577	US-08-658-136-1	Sequence 1, Appl1
18	16.4	78.1	677	US-08-896-164-42	Sequence 42, Appl1
19	16.4	78.1	1347	US-08-896-164-84	Sequence 84, Appl1
20	16.4	78.1	2297	US-09-799-451-689	Sequence 689, App
21	16.4	78.1	2630	US-08-669-286-6	Sequence 6, Appl1
22	16.4	78.1	2630	US-09-469-253-6	Sequence 6, Appl1
23	16.4	78.1	2630	US-09-642-146-6	Sequence 6, Appl1
24	16.4	78.1	8931	US-09-051-019-1	Sequence 1, Appl1
25	16.2	77.1	59	US-08-797-689-26	Sequence 26, Appl1
26	16.2	77.1	59	US-09-984-186-26	Sequence 26, Appl1
27	16.2	77.1	60	US-08-797-689-9	Sequence 7, Appl1

c	28	16.2	77.1	60	2	US-08-797-689-27	Sequence 27, Appl1
c	29	16.2	77.1	60	4	US-09-984-186-7	Sequence 7, Appl1
c	30	16.2	77.1	60	4	US-09-984-186-37	Sequence 27, Appl1
c	31	16.2	77.1	120	4	US-09-270-767-26922	Sequence 26922, A
c	32	16.2	77.1	288	4	US-08-797-689-9	Sequence 9, Appl1
c	33	16.2	77.1	288	4	US-09-984-186-9	Sequence 9, Appl1
c	34	16.2	77.1	509	4	US-09-621-976-14709	Sequence 14709, A
c	35	16.2	77.1	557	4	US-10-101-464A-168	Sequence 168, App
c	36	16.2	77.1	628	4	US-09-270-767-11361	Sequence 11361, A
c	37	16.2	77.1	681	3	US-08-347-584A-3	Sequence 3, Appl1
c	38	16.2	77.1	681	3	US-08-463-682-18	Sequence 18, Appl1
c	39	16.2	77.1	750	2	US-08-797-689-3	Sequence 3, Appl1
c	40	16.2	77.1	750	4	US-09-984-186-3	Sequence 3, Appl1
c	41	16.2	77.1	837	3	US-09-123-492A-3	Sequence 3, Appl1
c	42	16.2	77.1	925	4	US-09-311-021-119	Sequence 119, App
c	43	16.2	77.1	936	4	US-09-416-509C-2	Sequence 2, Appl1
c	44	16.2	77.1	960	2	US-07-841-591A-1	Sequence 1, Appl1
c	45	16.2	77.1	960	5	PCT-US93-02034-1	Sequence 1, Appl1

ALIGNMENTS

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RESULT 1
US-09-372-339-1
; Sequence 1, Application US/09372339
; Patent No. 6174684
; GENERAL INFORMATION:
; APPLICANT: Rebeck, Timothy
; TITLE OF INVENTION: CYP3A4 NFSE Variant and Methods of Use Therefor
; FILE REFERENCE: PENN-0695
; CURRENT FILING DATE: 1999-08-11
; EARLIER APPLICATION NUMBER: US/09/372,339
; EARLIER FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-372-339-1

Query Match      84.8%; Score 17.8; DB 3; Length 1345;
Best Local Similarity 90.5%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy      1  |||||
Db      1050 CTGCAGCCCTCCTCTCTCTC 1070

RESULT 2
US-09-372-339-2
; Sequence 2, Application US/09372339
; Patent No. 6174684
; GENERAL INFORMATION:
; APPLICANT: Rebeck, Timothy
; TITLE OF INVENTION: CYP3A4 NFSE Variant and Methods of Use Therefor
; FILE REFERENCE: PENN-0695
; CURRENT FILING DATE: 1999-08-11
; EARLIER APPLICATION NUMBER: US/09/372,339
; EARLIER FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-372-339-2
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Query Match 84.8%; Score 17.8; DB 3; Length 1345;
Best Local Similarity 90.5%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCAGCCCGCCCTCTTCTC 21
Db 1050 CTCGAGCCCTGCGCTCTTCTC 1070

RESULT 3

US-09-144-367-3
Sequence 3, Application US/09144367
Patent No. 6432639
GENERAL INFORMATION:
APPLICANT: Lichter, Jay
APPLICANT: Guido, Marco
TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
FILE REFERENCE: SEQ-12P
CURRENT APPLICATION NUMBER: US/09/144,367
CURRENT FILING DATE: 1998-08-31
PRIOR APPLICATION NUMBER: 60/058,612
PRIOR FILING DATE: 1997-09-10
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 1345
TYPE: DNA
ORGANISM: H. sapiens
FEATURE:
NAME/KEY: Other
LOCATION: (0)...(0)
US-09-144-367-3

Query Match 84.8%; Score 17.8; DB 4; Length 1345;
Best Local Similarity 90.5%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCAGCCCGCCCTCTTCTC 21
Db 1050 CTCGAGCCCTGCGCTCTTCTC 1070

RESULT 4

US-08-480-474-10/c
Sequence 10, Application US/08480474
Patent No. 6033865
GENERAL INFORMATION:
APPLICANT: Daggett, Lorie P.
APPLICANT: Ellis, Steven B.
APPLICANT: Liaw, Chen W.
APPLICANT: Lu, Chin-Chun
TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR SUBUNITS, DNA ENCODING
TITLE OF INVENTION: SAME AND USES THEREFOR
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUNTRY: U.S.A.
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,474
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie

REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9382B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 3545 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
US-08-480-474-10

Query Match 82.9%; Score 17.4; DB 3; Length 3545;
Best Local Similarity 94.7%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCAGCCCGCCCTCTTCTC 21
Db 500 GCAGCCCGCCCGCTCTCTC 482

RESULT 5

US-09-270-767-29245/c
Sequence 29245, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 29245
LENGTH: 189
TYPE: DNA
ORGANISM: Drosophila melanogaster
US-09-270-767-29245

Query Match 80.0%; Score 16.8; DB 4; Length 189;
Best Local Similarity 90.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCAGCCCGCCCTCTTCT 20
Db 176 CTGCAGATCCGCTCTTCT 157

RESULT 6

US-09-270-767-13305/c
Sequence 13305, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13305
LENGTH: 743
TYPE: DNA
ORGANISM: Drosophila melanogaster
US-09-270-767-13305

Query Match 80.0%; Score 16.8; DB 4; Length 743;
Best Local Similarity 90.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCAGCCCGCCCTCTTCT 20

Db 176 CTGCAGATCCGCCCTCTTCT 157

RESULT 7

US-07-863-169A-4
; Sequence 4, Application US/07863169A
; Patent No. 5420245
GENERAL INFORMATION:
APPLICANT: Brown, Michael S.
APPLICANT: Goldstein, Joseph L.
APPLICANT: Reiss, Yuval
TITLE OF INVENTION: Retriapeptide-Based Inhibitors of Farnesyl
TITLE OF INVENTION: Transferrase
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/863.169A
FILING DATE: 03-APR-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/822,011
FILING DATE: 19-JAN-1992
CLASSIFICATION: 530
APPLICATION NUMBER: US 07/937,893
FILING DATE: 18-APR-1991
CLASSIFICATION: 530
APPLICATION NUMBER: US 615,715
FILING DATE: 20-NOV-1990
CLASSIFICATION: 530
APPLICATION NUMBER: US 510,706
FILING DATE: 18-APR-1990
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTSD:297/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2464 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-07-863-169A-4

Query Match 80.0%; Score 16.8; DB 1; Length 2464;
Best Local Similarity 90.0%; Pred. No. 3e+02; 2; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCAGCCCCGCTCTTCT 20
Db 2146 CTGCAGCCCGAGCTCTTCT 2165

RESULT 8
US-08-429-964-4
; Sequence 4, Application US/08429964
; Patent No. 5962243

GENERAL INFORMATION:
APPLICANT: BROWN, MICHAEL S.
APPLICANT: GOLDSTEIN, JOSEPH L.
APPLICANT: REISS, YUVAL
TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF FARNESYL
TITLE OF INVENTION: TRANSFERASE INHIBITORS
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESSES:
ADDRESSEE: ARNOLD, WHITE & DURKEE
STREET: P.O. BOX 4433
CITY: HOUSTON
STATE: TEXAS
COUNTRY: UNITED STATES OF AMERICA
ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,964
FILING DATE: 27-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/021,625
FILING DATE: 16-FEB-1993
CLASSIFICATION: 435
APPLICATION NUMBER: US 07/822,011
FILING DATE: ABANDONED
CLASSIFICATION: 435
APPLICATION NUMBER: PCT/US/91/02650
FILING DATE: 18-APR-1991
CLASSIFICATION: 435
APPLICATION NUMBER: US 07/615,715
FILING DATE: 20-NOV-1990
CLASSIFICATION: 435
APPLICATION NUMBER: US 07/510,706
FILING DATE: 18-APR-1990 (ABANDONED)
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PARKER, DAVID L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTSD:432/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2464 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-429-964-4

Query Match 80.0%; Score 16.8; DB 2; Length 2464;
Best Local Similarity 90.0%; Pred. No. 3e+02; 2; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCAGCCCCGCTCTTCT 20
Db 2146 CTGCAGCCCGAGCTCTTCT 2165

RESULT 9
US-07-935-087-4
; Sequence 4, Application US/07935087
; Patent No. 6083917
GENERAL INFORMATION:
APPLICANT: BROWN, MICHAEL S.
APPLICANT: GOLDSTEIN, JOSEPH L.
APPLICANT: REISS, YUVAL

```

1 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
2 TITLE OF INVENTION: THE IDENTIFICATION,
3 TITLE OF INVENTION: CHARACTERIZATION,
4 TITLE OF INVENTION: AND INHIBITION OF PARNESTYL
5 TITLE OF INVENTION: PROTEIN TRANSFERASE
6 NUMBER OF SEQUENCES: 8
7 CORRESPONDENCE ADDRESS:
8 ADDRESS: ARNOLD, WHITE & DURKEE
9 STREET: P.O. BOX 4433
10 CITY: HOUSTON
11 STATE: TEXAS
12 COUNTRY: USA
13 ZIP: 77210
14
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: FLOPPY DISK
17 COMPUTER: IBM PC COMPATIBLE
18 OPERATING SYSTEM: PC-DOS/MS-DOS
19 SOFTWARE: WORDPERFECT 5.1 (converted to ASCII-DOS)
20
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/07/935,087
23 FILING DATE: 19920824
24 CLASSIFICATION: 435
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: US/07/822,011
27 FILING DATE: 01/16/92
28 ATTORNEY/AGENT INFORMATION:
29 NAME: PARKER, DAVID L.
30 REGISTRATION NUMBER: 32,165
31 REFERENCE/DOCKET NUMBER: UTS&D:269/P&R
32 TELECOMMUNICATION INFORMATION:
33 TELEPHONE: 512-320-7200
34 TELEFAX: 512-474-7577
35
36 TELEX:
37 INFORMATION FOR SEQ ID NO: 4:
38 SEQUENCE CHARACTERISTICS:
39 LENGTH: 2464 base pairs
40 TYPE: nucleic acid
41 STRANDEDNESS: single
42 TOPOLOGY: linear
43
44 US-07-935-087-4
45
46 Query Match 80.0%; Score 16.8; DB 3; Length 2464;
47 Best Local Similarity 90.0%; Pred. No. 3e+02;
48 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
49
50 QY 1 CTGCAGCCCGCCTCTCTTCT 20
51 ||||||| |||||||
52 Db 2146 CTGCAGCCCGCAGCTCTCTTCT 2165
53
54 RESULT 10
55 FCT-US93-08062-4
56 Sequence 4, Application PC/TUS9308062
57 GENERAL INFORMATION:
58 APPLICANT:
59 SEQUENCE CHARACTERISTICS: BROWN, MICHAEL S.
60 SEQUENCE CHARACTERISTICS: GOLDSTEIN, JOSEPH L.
61 SEQUENCE CHARACTERISTICS: REISS, YUVAL
62 SEQUENCE CHARACTERISTICS: MASTERS, JR., JAMES C.
63 ADDRESS: METHODS AND COMPOSITIONS FOR
64 ADDRESS: THE IDENTIFICATION,
65 ADDRESS: CHARACTERIZATION AND
66 ADDRESS: INHIBITION OF
67 ADDRESS: PARNESTYLTRANSFERASE
68 NUMBER OF SEQUENCES: 71
69 CORRESPONDENCE ADDRESS:
70 ADDRESS: ARNOLD, WHITE & DURKEE
71 STREET: P.O. BOX 4433
72 CITY: HOUSTON
73 STATE: TEXAS
74 COUNTRY: UNITED STATES OF AMERICA
75 ZIP: 77210

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: COMPUTER READABLE FORM:
: MEDIUM TYPE: FLOPPY DISK/ASKII
: COMPUTER: IBM PC COMPATIBLE
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WORDPERFECT 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US93/08062
: FILING DATE: AUGUST 24, 1993
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/935,087
: FILING DATE: 24 AUGUST 1992 (24.08.92)
: NAME: UNKNOWN
: ATTORNEY/AGENT INFORMATION:
: NAME: PARKER, DAVID L.
: REGISTRATION NUMBER: 32,165
: REFERENCE/DOCKET NUMBER: UHF0377PCT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 512-320-7200
: TELEFAX: 512-474-7577
: TELEX: NOT APPLICABLE
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2464 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: PCT-US93-08062-4

Query Match      80.0%; Score 16.8; DB 5; Length 2464;
Best Local Similarity 90.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0.

QY      1 CTGCAGCCCCGCTCTCTTCT 20
DB      2146 CTGCAGCCCGAGCTCTCTTCT 2165

RESULT 11
US-09-917-254-40/c
: Sequence 40, Application US/09917254
: Patent No. 6703204
: GENERAL INFORMATION:
: APPLICANT: Mutter, George
: APPLICANT: Baak, Jan
: TITLE OF INVENTION: Prognostic Classification of Breast Cancer
: FILE REFERENCE: B0801/7224(JRV)
: CURRENT APPLICATION NUMBER: US/09/917,254
: CURRENT FILING DATE: 2001-07-27
: PRIOR APPLICATION NUMBER: US 60/222,093
: PRIOR FILING DATE: 2000-07-28
: NUMBER OF SEQ ID NOS: 102
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 40
: LENGTH: 5574
: TYPE: DNA
: ORGANISM: Homo Sapiens
US-09-917-254-40

Query Match      80.0%; Score 16.8; DB 4; Length 5574;
Best Local Similarity 90.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CTGCAGCCCCGCTCTCTTCT 20
DB      2934 CTGCAGCTCTCTCTCTTCT 2915

RESULT 12
US-09-620-312D-248/c
: Sequence 248, Application US/09620312D
: Patent No. 6569662
: GENERAL INFORMATION:

```

APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yundong
APPLICANT: Wang, Dunwei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 656962e1 Nucleic Acids and
FILE REFERENCE: 784CIP28
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: PL_genes Version 1.0
SEQ ID NO 248
LENGTH: 7453
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(4362)
US-09-620-312D-248

Query Match 80.0%; Score 16.8; DB 4; Length 7453;
Best Local Similarity 90.0%; Pred. No. 3e+02; 2; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0;

Qy 1 CTGCAGCCCGCCTCTTCT 20
Db 3279 CTGCAGCTCCTCCTCTTCT 3260
RESULT 13
US-09-620-312D-249/c
Sequence 249, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yundong
APPLICANT: Wang, Dunwei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 656962e1 Nucleic Acids and
FILE REFERENCE: 784CIP28
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19

PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: PL_genes Version 1.0
SEQ ID NO 249
LENGTH: 7501
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(4410)
US-09-620-312D-249

Query Match 80.0%; Score 16.8; DB 4; Length 7501;
Best Local Similarity 90.0%; Pred. No. 3e+02; 2; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0;

Qy 1 CTGCAGCCCGCCTCTTCT 20
Db 3327 CTGCAGCTCCTCCTCTTCT 3308

RESULT 14
US-09-023-655-1463/c
Sequence 1463, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Sellhammer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREMITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1463:
SEQUENCE CHARACTERISTICS:
LENGTH: 7596 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 9641957
US-09-023-655-1463

GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

Run on: January 26, 2005, 13:15:32 ; Search time 148.867 Seconds
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Title: US-10-085-612A-24
Perfect score: 21
Sequence: 1 ctgcagcccccctctctc 21

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues
Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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11: /cgn2_6/prodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/prodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/prodata/1/pubpna/US10E_PUBCOMB.seq:*
17: /cgn2_6/prodata/1/pubpna/US10F_PUBCOMB.seq:*
18: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq:*
19: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq:*
20: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq:*
21: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19.4	92.4	1254	14	US-10-085-612-4
2	18.4	87.6	1142	18	US-10-425-115-95740
3	17.8	84.8	162	16	US-10-260-238-5770
4	17.8	84.8	235	17	US-10-437-963-39436
5	17.8	84.8	333	17	US-10-437-963-4246
6	17.8	84.8	907	17	US-10-767-701-9673
7	17.8	84.8	1012	9	US-09-957-997-4
8	17.8	84.8	1080	16	US-10-282-122A-14967
9	17.8	84.8	1115	17	US-10-437-963-4245
10	17.8	84.8	1286	16	US-10-425-114-25053
11	17.8	84.8	1294	18	US-10-425-115-33839
12	17.8	84.8	1345	10	US-09-943-115A-1

13	17.8	84.8	1345	14	US-10-146-575-3	Sequence 3, Appl1
14	17.8	84.8	1345	18	US-10-085-612-3	Sequence 3, Appl1
15	17.8	84.8	1471	18	US-10-425-115-20894	Sequence 20894, A
16	17.8	84.8	2374	5	US-10-094-749-173	Sequence 173, App
17	17.8	84.8	11186	9	US-09-957-997-1	Sequence 1, Appl1
18	17.8	84.8	13035	15	US-10-121-960C-14	Sequence 14, Appl1
19	17.8	84.8	15185	15	US-10-121-960C-17	Sequence 17, Appl1
20	17.8	84.8	29560	17	US-10-322-281-791	Sequence 791, App
21	17.8	84.8	136284	17	US-10-775-169-149	Sequence 149, App
22	17.8	84.8	227246	17	US-10-322-281-314	Sequence 314, App
23	17.4	82.9	503	9	US-09-783-590-5595	Sequence 5595, App
24	17.4	82.9	555	17	US-10-437-963-38151	Sequence 38151, A
25	17.4	82.9	685	17	US-10-767-701-27580	Sequence 27580, A
26	17.4	82.9	1212	18	US-10-193-452-18	Sequence 18, Appl1
27	17.4	82.9	1902	18	US-10-193-452-16	Sequence 16, Appl1
28	17.4	82.9	2376	17	US-10-437-963-53218	Sequence 53218, A
29	17.4	82.9	3687	17	US-10-437-963-94562	Sequence 94562, A
30	17.4	81.0	21581	15	US-10-017-161-2041	Sequence 2041, App
31	17	81.0	21581	15	US-10-292-798-1687	Sequence 1687, App
32	17	81.0	53542	9	US-09-801-574-61	Sequence 61, Appl1
33	16.8	80.0	201	17	US-10-741-601-1452	Sequence 1452, App
34	16.8	80.0	201	17	US-10-741-601-1495	Sequence 1495, App
35	16.8	80.0	326	13	US-10-027-632-267839	Sequence 267839, A
36	16.8	80.0	326	15	US-10-027-632-267839	Sequence 267839, A
37	16.8	80.0	330	18	US-10-425-115-27622	Sequence 27622, A
38	16.8	80.0	425	9	US-09-796-592-5944	Sequence 5944, App
39	16.8	80.0	425	16	US-10-040-862-5944	Sequence 5944, App
40	16.8	80.0	425	16	US-10-057-475B-5944	Sequence 5944, App
41	16.8	80.0	425	16	US-10-154-884B-5944	Sequence 5944, App
42	16.8	80.0	477	17	US-10-764-324-5944	Sequence 5944, App
43	16.8	80.0	477	10	US-09-918-995-12275	Sequence 12275, A
44	16.8	80.0	489	10	US-09-918-995-26537	Sequence 26537, A
45	16.8	80.0	508	15	US-10-029-386-6894	Sequence 6894, App

ALIGNMENTS

RESULT 1
US-10-085-612-4
Sequence 4, Application US/10085612
Publication No. US20030096251A1
GENERAL INFORMATION:
APPLICANT: Guida, Marco
APPLICANT: Hall, Jeff
APPLICANT: Petros, William
APPLICANT: Vredenburg, James
APPLICANT: Colvin, Oliver
APPLICANT: Marks, Jeffrey
TITLE OF INVENTION: Methods for Evaluating the Ability to Metabolize Pharmaceuticals
FILE REFERENCE: 4389-5-CT
CURRENT APPLICATION NUMBER: US/10/085,612
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 09/144,367
PRIOR FILING DATE: 1998-08-31
PRIOR APPLICATION NUMBER: 60/271,630
PRIOR FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 1254
TYPE: DNA
ORGANISM: Homo sapiens
US-10-085-612-4
Query Match 92.4%; Score 19.4; DB 14; Length 1254;
Best Local Similarity 95.2%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CY 1 CTGCAGCCCGCCTCTCTC 21
DB 1027 CTGCAGCCCGCCTCTCTC 1047

RESULT 2

US-10-425-115-95740
; Sequence 95740, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 95740
; LENGTH: 1142
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_18829C.1
US-10-425-115-95740

Query Match 87.6%; Score 18.4; DB 18; Length 1142;
Best Local Similarity 95.0%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CTGAGCGCCGCTCTTCT 20
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Db 519 CTGAGCGCCGCTCTTCT 538
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RESULT 3

US-10-260-238-5770
; Sequence 5770, Application US/10260238
; Publication No. US20040016025A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, Paul R.
; APPLICANT: Moughamer, Todd G.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazedbrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyaki
; APPLICANT: Kieps, Joel
; APPLICANT: Provart, Nicholas
; APPLICANT: Ricke, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
; FILE REFERENCE: 60111-NP
; CURRENT APPLICATION NUMBER: US/10/260,238
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/325,448
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 6077
; SEQ ID NO 5770
; LENGTH: 162
; TYPE: DNA
; ORGANISM: Zea mays
US-10-260-238-5770

Query Match 84.8%; Score 17.8; DB 16; Length 162;
Best Local Similarity 90.5%; Pred. No. 3.5e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CTGAGCGCCGCTCTTCT 21
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Db 48 CTTCAGCCGCGCTCTTCT 68
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RESULT 4

US-10-437-963-39436/C
; Sequence 39436, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 39436
; LENGTH: 235
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_42977C.1
US-10-437-963-39436

Query Match 84.8%; Score 17.8; DB 17; Length 235;
Best Local Similarity 90.5%; Pred. No. 3.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CTGAGCGCCGCTCTTCT 21
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Db 209 CTTCAGCCGCGCTCTTCT 189
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RESULT 5

US-10-437-963-4246/C
; Sequence 4246, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 4246
; LENGTH: 333
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_11147C.1
US-10-437-963-4246

Query Match 84.8%; Score 17.8; DB 17; Length 333;
Best Local Similarity 90.5%; Pred. No. 3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CTGAGCGCCGCTCTTCT 21
|||

Db 36 CTGAGCTCGCGCTCTTCT 16
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RESULT 6
US-10-767-701-9673/c
; Sequence 9673, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 9673
; LENGTH: 907
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS29634_1
; US-10-767-701-9673

Query Match      84.8%; Score 17.8; DB 17; Length 907;
Best Local Similarity 90.5%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CTGCAGCCCGCCCTCTCTC 21
        |||||
Db      172 CTGCAGCTCCGCGCCCTCTCTC 152

RESULT 7
US-09-957-997-4
; Sequence 4, Application US/09957997
; Patent No. US20020150915A1
; GENERAL INFORMATION:
; APPLICANT: Berkenstam, Anders
; APPLICANT: Bertilsson, Gran
; APPLICANT: Blomquist, Patrik
; TITLE OF INVENTION: PROMOTER SEQUENCES
; FILE REFERENCE: 13425-046001
; CURRENT APPLICATION NUMBER: US/09/957,997
; CURRENT FILING DATE: 2001-09-21
; EARLIER APPLICATION NUMBER: SE 0003393-6
; EARLIER FILING DATE: 2000-09-22
; EARLIER APPLICATION NUMBER: 60/238,895
; EARLIER FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1012
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-957-997-4

Query Match      84.8%; Score 17.8; DB 9; Length 1012;
Best Local Similarity 90.5%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CTGCAGCCCGCCCTCTCTC 21
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Db      962 CTCGAGCCCTGCTCTCTCTC 982

RESULT 8
US-10-282-122A-14967/c
; Sequence 14967, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
```

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; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zykkind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; CURRENT APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14967
; LENGTH: 1080
; TYPE: DNA
; ORGANISM: Bordetella pertussis
; US-10-282-122A-14967

Query Match      84.8%; Score 17.8; DB 16; Length 1080;
Best Local Similarity 90.5%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CTGCAGCCCGCCCTCTCTC 21
        |||||
Db      291 CTGCAGCGCGCCCTCCATCTC 271

RESULT 9
US-10-437-963-4245/c
; Sequence 4245, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 4245
; LENGTH: 1115
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TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_11146C.1
US-10-437-963-4245

Query Match 84.8%; Score 17.8; DB 17; Length 1115;
Best Local Similarity 90.5%; Pred. No. 2.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCAGCCCGCCTCTTCTC 21
Db 191 CTGCAGCTCCGCGCCTTCTC 171

RESULT 10
US-10-425-114-25053/C
Sequence 25053, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E.

APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 25053
LENGTH: 1286
TYPE: DNA
ORGANISM: Zea mays

FEATURE:
OTHER INFORMATION: Clone ID: LIB3689-241-G6_FLI

US-10-425-114-25053

Query Match 84.8%; Score 17.8; DB 16; Length 1286;
Best Local Similarity 90.5%; Pred. No. 2.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCAGCCCGCCTCTTCTC 21
Db 156 CTTCAGCCCGCCTCTTCTC 136

RESULT 11
US-10-425-115-33839/C
Sequence 33839, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 33839
LENGTH: 1294
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_130869C.1
US-10-425-115-33839

Query Match 84.8%; Score 17.8; DB 18; Length 1294;

Best Local Similarity 90.5%; Pred. No. 2.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCAGCCCGCCTCTTCTC 21
Db 1146 CTGCAGCCCGCCTCTTCTC 1126

RESULT 12
US-09-943-115A-1
Sequence 1, Application US/09943115A
Publication No. US20030017469A1
GENERAL INFORMATION:
APPLICANT: SEQUENOM, Inc.
APPLICANT: Risinger, Carl
APPLICANT: Anderson, Maria
APPLICANT: Lewander, Tommy
APPLICANT: Olaisen, Erik

TITLE OF INVENTION: DETECTION OF CYP3A4 AND CYP2C9
TITLE OF INVENTION: POLYMORPHISMS
FILE REFERENCE: 52459-20021.00
CURRENT APPLICATION NUMBER: US/09/943,115A
CURRENT FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: UK 0021286.0
PRIOR FILING DATE: 2000-08-30

NUMBER OF SEQ ID NOS: 73
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1345
TYPE: DNA
ORGANISM: Homo sapiens
US-09-943-115A-1

Query Match 84.8%; Score 17.8; DB 10; Length 1345;
Best Local Similarity 90.5%; Pred. No. 2.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCAGCCCGCCTCTTCTC 21
Db 1050 CTTCAGCCCTGCTCTTCTC 1070

RESULT 13
US-10-146-575-3
Sequence 3, Application US/10146575
Publication No. US20030059800A1
GENERAL INFORMATION:
APPLICANT: Lichter, Jay
APPLICANT: Guido, Marco

TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
FILE REFERENCE: SEQ-12P
CURRENT APPLICATION NUMBER: US/10/146,575
CURRENT FILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: US/09/144,367
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 1345
TYPE: DNA
ORGANISM: H. sapiens
FEATURE:
NAME/KEY: Other
LOCATION: (0)...(0)
US-10-146-575-3

Query Match 84.8%; Score 17.8; DB 14; Length 1345;
Best Local Similarity 90.5%; Pred. No. 2.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCAGCCCGCCTCTTCTC 21
Db 1050 CTTCAGCCCTGCTCTTCTC 1070

RESULT 14

US-10-085-612-3
; Sequence 3, Application US/10085612
; Publication No. US20030096251A1
; GENERAL INFORMATION:
; APPLICANT: Guida, Marco
; APPLICANT: Hall, Jeff
; APPLICANT: Petros, William
; APPLICANT: Vredenburgh, James
; APPLICANT: Colvin, Oliver
; APPLICANT: Marks, Jeffrey
; TITLE OF INVENTION: Methods for Evaluating the Ability to Metabolize Pharmaceuticals
; FILE REFERENCE: 4389-5-C1
; CURRENT APPLICATION NUMBER: US/10/085,612
; PRIOR FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/144,367
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/271,630
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-612-3

Query Match 84.8%; Score 17.8; DB 14; Length 1345;
Best Local Similarity 90.5%; Pred. No. 2.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCAGCCCGCCCTCTCTC 21

Db 1050 CTGCAGCCCTGCTCTCTCTC 1070

RESULT 15

US-10-425-115-20894/C
; Sequence 20894, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yinhua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 20894
; LENGTH: 1471
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MFT4577_119054C.1
US-10-425-115-20894

Query Match 84.8%; Score 17.8; DB 18; Length 1471;
Best Local Similarity 90.5%; Pred. No. 2.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCAGCCCGCCCTCTCTC 21

Db 285 CTGCAGCCCGCCCTCTCTC 265

Search completed: January 26, 2005, 18:15:54
Job time : 149.867 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 26, 2005, 13:23:32 ; Search time 103.779 Seconds
(without alignments)
8588.699 Million cell updates/sec

Title: SEQ4-1037G
Perfect score: 1254
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq: *
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	499.2	39.8	1345	US-09-372-339-2	Sequence 2, Appl1
2	498.8	39.8	1345	US-09-144-367-3	Sequence 3, Appl1
3	497.6	39.7	1345	US-09-372-339-1	Sequence 1, Appl1
4	142	11.3	1707	US-09-023-655-1060	Sequence 1060, Ap
5	128.2	10.2	1599	US-09-023-655-1405	Sequence 1405, Ap
6	122.6	9.8	2059	US-09-023-655-1062	Sequence 1062, Ap
7	107.8	8.6	1659	US-09-583-447A-1	Sequence 1, Appl1
8	102.6	8.2	2759	US-09-144-367-1	Sequence 1, Appl1
9	89	7.1	105	US-09-583-447A-41	Sequence 41, Appl1
10	78.8	6.3	106	US-09-583-447A-40	Sequence 40, Appl1
11	77.2	6.2	106	US-09-583-447A-39	Sequence 39, Appl1
12	72.6	5.8	7218	US-08-232-463-14	Sequence 14, Appl1
13	61.4	4.9	1512	US-08-277-031B-4	Sequence 4, Appl1
14	61.2	4.9	106	US-09-583-447A-42	Sequence 42, Appl1
15	51	4.1	243	US-09-172-108-12	Sequence 12, Appl1
16	51	4.1	265	US-09-172-108-10	Sequence 10, Appl1
17	49.2	3.9	36159	US-09-749-588-3	Sequence 3, Appl1
18	49.2	3.9	36159	US-10-135-687-3	Sequence 3, Appl1
19	48.6	3.9	1192	US-09-583-447A-9	Sequence 9, Appl1
20	48.6	3.9	1349	US-09-583-447A-5	Sequence 5, Appl1
21	48.6	3.9	1515	US-09-583-447A-3	Sequence 3, Appl1
22	48.6	3.9	1633	US-09-583-447A-7	Sequence 7, Appl1
23	48.6	3.9	1972	US-09-583-447A-11	Sequence 11, Appl1
24	47.8	3.8	64467	US-09-803-671B-3	Sequence 3, Appl1
25	47.4	3.8	57	US-07-640-473-5	Sequence 5, Appl1
26	47.4	3.8	57	US-07-908-317-24	Sequence 24, Appl1
27	47.4	3.8	57	PCT-US93-06171-24	Sequence 24, Appl1

C	28	46.8	3.7	202001	4	US-09-734-674-3	Sequence 3, Appl1
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C	30	45.6	3.6	283	4	US-09-513-999C-30164	Sequence 30164, A
C	31	45.6	3.6	384	4	US-09-513-999C-30900	Sequence 30900, A
C	32	44.6	3.6	116592	4	US-09-818-512-3	Sequence 3, Appl1
C	33	44.2	3.5	57	1	US-07-640-473-13	Sequence 13, Appl1
C	34	44	3.5	13158	4	US-08-687-080-105	Sequence 105, App
C	35	42.6	3.4	57	1	US-07-640-473-7	Sequence 7, Appl1
C	36	42.6	3.4	57	1	US-07-640-473-11	Sequence 11, Appl1
C	37	42.6	3.4	57	1	US-07-908-317-26	Sequence 26, Appl1
C	38	42.6	3.4	57	5	PCT-US93-06171-26	Sequence 26, Appl1
C	39	42.2	3.4	551	3	US-08-896-164-38	Sequence 38, Appl1
C	40	41	3.3	57	1	US-07-640-473-9	Sequence 9, Appl1
C	41	40.8	3.3	107820	4	US-09-792-616-1	Sequence 1, Appl1
C	42	40	3.2	289	3	US-09-007-005-17	Sequence 17, Appl1
C	43	40	3.2	289	3	US-09-244-796-17	Sequence 17, Appl1
C	44	38.4	3.1	3286	3	US-09-211-417-2	Sequence 2, Appl1
C	45	38	3.0	786431	4	US-09-751-389-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1									
US-09-372-339-2									
Sequence 2, Application US/09372339									
Patent No. 6174684									
GENERAL INFORMATION:									
APPLICANT: Redbeck, Timothy									
FILE REFERENCE: PENN-0695									
TITLE OF INVENTION: CYP3A4 NFSE Variant and Methods of Use Therefor									
CURRENT FILING DATE: 1999-08-11									
EARLIER FILING DATE: 60/096,586									
NUMBER OF SEQ ID NOS: 6									
SOFTWARE: PatentIn Ver. 2.0									
SEQ ID NO 2									
LENGTH: 1345									
TYPE: DNA									
ORGANISM: Homo sapiens									
US-09-372-339-2									
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Best Local Similarity 77.8%; Pred. No. 4,56-158; Length 1345;									
Matches 710; Conservative 0; Mismatches 128; Indels 74; Gaps 6;									
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QY	462	CCACATGCTGTACAGTACCTCTGTGAGGTCACAGGTCATGAAATTAATCCAGAC	521						
DB	442	CCCACTGTGTACAGTACCTCTGTGAGGTCACAGGTCATGAAATTAATCCAGAC	501						
QY	522	TGCGCCCTTGAAGAACTCCTCTGTGAGGTCACAGGTCATGAAATTAATCCAGAC	581						
DB	502	TATGCCCTTGAAGAACTCCTCTGTGAGGTCACAGGTCATGAAATTAATCCAGAC	559						
QY	582	TAGAGAGAAATAGCAATAGCACTGTGAGGTCACAGGTCATGAAATTAATCCAGAC	641						
DB	560	TAAAGAGAAATAGCAATAGCACTGTGAGGTCACAGGTCATGAAATTAATCCAGAC	619						
QY	642	ATGTTTCACTGTGTGAGGTCATGAGGTCATGAAATTAATTAATGAGGCTGTCTG	701						
DB	620	ATGTTTCACTGTGTGAGGTCATGAGGTCATGAAATTAATTAATGAGGCTGTCTG	678						
QY	702	GTGGGCTTCAAGATGATGAGGTCATGAGGTCATGAAATTAATTAATGAGGCTGTCTG	761						
DB	679	TCGGGCTTCAAGATGATGAGGTCATGAGGTCATGAAATTAATTAATGAGGCTGTCTG	732						
QY	762	GGAATTCATGAGGTAAGATCTGAGTGTGAGGTCATGAGGTCATGAAATTAATTCG	821						

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Db 733 -----GCATAGGTAAGATCTGTAGGTTGGCTTGTGGATGAATTTCAAGATTTTG 786
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Db 787 GAATGAGACAGCCATGAGAAACAAGGACGCTGAGAGATTTAAAGATTTATCCA 846
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Qy 942 TTAAGTTGTTTATGATTTCCCATTAAGAACTCAAGAGGTAAAG-CAAGGGGTGT 1000
Db 907 TTGAGTTGTTTATGATTTCTCATTAAGAACTCAAGAGGTCAAGTGTGTGTGT 966
Qy 1001 GTGGATTTCTT----- 1011
Db 967 GTGTGATTTCTTGTCCAACTTCCAAAGTGGAGAAAGCTTTCCAACTGACGACAGACACA 1026
Qy 1012 -----TGCTACTGCTGCTGACGCTGACGCCGCTCTTCTTCCAGACATTAACAATTT 1063
Db 1027 GGTGGCCCTGCTAATGCTGCTGACGCTGACGCCGCTCTTCTTCTGATTAATTAACAATC 1086
Qy 1064 CAGAGCTTGAACCTAA-GACTGCTGTGTGAGGCGAGGATGCTCCAGGACAGACCCAGC 1122
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Qy 1183 GATGACCTCATCCCAATTTGGCGGTGAAACCTGGCTTCTCCGTGCTGTCAAGCTGTGT 1242
Db 1207 GATGACCTCATCCCAAGCTTGGCCATGGAACCTGGCTTCTCCGTGCTGTCAAGCTGTGT 1266
Qy 1243 GCTCCTCTATCT 1254
Db 1267 GCTCCTCTATCT 1278

RESULT 2
US-09-144-367-3
; Sequence 3, Application US/09144367
; Patent No. 6432639
; GENERAL INFORMATION:
; APPLICANT: Lichter, Jay
; APPLICANT: Guido, Marco
; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
; FILE REFERENCE: SEQ-12P
; CURRENT APPLICATION NUMBER: US/09/144,367
; CURRENT FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/058,612
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: Other
; LOCATION: (0)...(0)
; US-09-144-367-3
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Query Match 39.8%; Score 498.8; DB 4; Length 1345;
Best Local Similarity 77.7%; Pred. No. 6.2e-158;
Matches 709; Conservative 1; Mismatches 128; Indels 74; Gaps 6;
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Qy 402 GGATGACACACAGGCGCCAGCAATTCACCAAGTCACTCCACCAACATTTCTGGTCA 461
Db 382 GGAATGACACAGGCGCCAGCAATTCACCAAGTCACTCCACCAACATTTCTGGTCA 441
Qy 462 CCACCATGTGTACAGTACCTGCTAAGGCTCAGGGTCAAGAAAGTAAATATACACAGAC 521
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Db 442 CCACATGTGTACAGTACCTGCTAAGGCTCAGGGTCAAGAAAGTAAATATACAGTAC 501
Qy 522 TGGGCCCTTAAAGAACTCACTGCTTAAGGAAACAGGACACAGAAACCCACAAGGGTGG 581
Db 502 TATGCCCTTAAAGAACTCACTGCTTAAAGGAAACAGGACAGGAGTGGAA--CACAATGGTGG 559
Qy 582 TAGAGAGAAATAGACCAATAGACCTGTGTAGAGGGGATAGAGGACCCAGAGAGAGAA 641
Db 560 TAAAGAGAAATAGAGCAATAGATAGTATGAAAGGGGATAGAGAGTCCAGAGGAGAGAA 619
Qy 642 ATGTTTACATCTGTGTAGAGAGGTTGGTAAAGAAAGCTTTAATAGAGGGGTCTGTCTG 701
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Qy 702 GCTGGCTTCAAGAGATGTGTAGAGAGTCACTAGGGGGCACAAGTACATCCAGGACAGAG 761
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Qy 762 GGAATTCATGAGTAAAGATCTGCAAGTGTGCTGTGGGATAGATTTCAAGTATTTCTG 821
Db 733 -----GCATAGGTAAGATCTGTAGGTTGGCTTGTGGGATGAATTTCAAGTATTTTG 786
Qy 822 GAATGAGACAGCCATGAGAAACAAGGACGCTGAGAGATTTAAAGGCTTATCCA 881
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Qy 882 ATGGCTCAGCTTCACTGATTTGATTAAGAACTCAGGTTCCGTGACTCCCTGATTAAGTGA 941
Db 847 ATGGCTCAGCTTCACTGATTTGATTAAGAACTCAGGTTCCGTGACTCCCTGATTAAGTGA 906
Qy 942 TTAAGTTGTTTATGATTTCCCATTAAGAACTCAAGAGGTAAAG-CAAGGGGTGT 1000
Db 907 TTGAGTTGTTTATGATTTCTCATTAAGAACTCAAGAGGTCAAGTGTGTGTGT 966
Qy 1001 GTGGATTTCTT----- 1011
Db 967 GTGTGATTTCTTGTCCAACTTCCAAAGTGGAGAAAGCTTTCCAACTGACGACAGACACA 1026
Qy 1012 -----TGCTACTGCTGCTGACGCTGACGCCGCTCTTCTTCCAGACATTAACAATTT 1063
Db 1027 GGTGGCCCTGCTAATGCTGCTGACGCTGACGCCGCTCTTCTTCTGATTAATTAACAATC 1086
Qy 1064 CAGAGCTTGAACCTAA-GACTGCTGTGTGAGGCGAGGATGCTCCAGGACAGACCCAGC 1122
Db 1087 CAACAGCCTCACTGAATCACTGTGTGAGGCGAGGAAAGCTCCATGACATACCCAGC 1146
Qy 1123 AAACAAGACACACAGCTGAAGTAAGTCACTGAGAGACAGCTGAAGAAAGGCAAGTGGC 1182
Db 1147 AAACAAGACACACAGCTGAAGTAAGTCACTGAGAGAGATTAAGTAAGAAAGTAAAGT 1206
Qy 1183 GATGACCTCATCCCAATTTGGCGGTGAAACCTGGCTTCTCCGTGCTGTCAAGCTGTGT 1242
Db 1207 GATGACCTCATCCCAAGCTTGGCCATGGAACCTGGCTTCTCCGTGCTGTCAAGCTGTGT 1266
Qy 1243 GCTCCTCTATCT 1254
Db 1267 GCTCCTCTATCT 1278
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RESULT 3
US-09-372-339-1
; Sequence 1, Application US/09372339
; Patent No. 6174684
; GENERAL INFORMATION:
; APPLICANT: Rebbeck, Timothy
; APPLICANT: Felix, Carolyn
; TITLE OF INVENTION: CYP3A4 NFSE Variant and Methods of Use Therefor
; FILE REFERENCE: PENN-0695
; CURRENT APPLICATION NUMBER: US/09/372,339
; CURRENT FILING DATE: 1999-08-11
; EARLIER APPLICATION NUMBER: 60/096,586
; EARLIER FILING DATE: 1998-08-14
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NUMBER OF SEQ ID NOS: 6
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 1
 LENGTH: 1345
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-372-339-1

Query Match 39.7%; Score 497.6; DB 3; Length 1345;
 Best Local Similarity 77.7%; Pred. No. 1.6e-157;
 Matches 709; Conservative 0; Mismatches 129; Indels 74; Gaps 6;

QY 402 GGATGACACACAGGGGCCAGCAATCTCACCAAGTCACTCCACCAATTTCTGTCTCA 461
 DB 382 GGATGACATAGCAGGCCCAAGCAATCTCAGTAACTCACTCCAGCCCTTTCTAGTTG 441
 QY 462 CCCACCATGTGTACAGTACCTCTCTAGGGTCCAGGGTCATGAAAGTAAATATACAGAC 521
 DB 442 CCCACTGTGTACAGCACCCTGTAGGGACAGAGCATGACAGGGAATTAAGCTAGAC 501
 QY 522 TGTGCTTGAAGAACTCACTCTCTCTAAGGAAACAGGCAAGCAAGGAGTGG 581
 DB 502 TATGCCCTTGAAGAGCTCCTCTCTCAGGAAACAGGGGTGAA--CACAATGTGG 559
 QY 582 TAGAGAGAAATAGACATAGAGCTGTGAGGGGATAGAGGACCCAGAGAGAA 641
 DB 560 TAAAGAGAAAGAGACATAGATTCATGAGGATGAAAAGTCCCAAGGGAGAA 619
 QY 642 ATGGTTACATCTGTGTAGAGAGGTGTGTAAGAAAGCTTAAATAGAGGGTCTGTG 701
 DB 620 ATGTTACATCTGTGTAGAGAGGTGTGTAAGAAAGCTTAAAGAA--GGCTCTGTG 678
 QY 702 GCTGGCTTGAAGAGATGTAGAGCTCTAGGGGCAAGTAACTCCAGGCGAG 761
 DB 679 TCTGGGTTGAAAGAGTGTAGAGCTTCTAGGGGCAAGGCACTCCAG----- 732
 QY 762 GGAATTCATGAGTAAAGATCTCAGTGTGCTTGTGGGAGATGATTTCAAGATTCTG 821
 DB 733 -----GCATAGTAAAGATCTGAGTGTGCTTGTGGAGTAAATTTCAAGATTCTG 786
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 DB 787 GAATGAGACAGCCATGAGAAACAGGGCAGGCAAGAGGCAATTTAATATATCCCA 846
 QY 882 ATGGCTTCACTTCACTTCTGATTAAGAACTCAGGTTCCCTGAGTCTCTGATTAAGTGA 941
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 QY 942 TTAAGTTGTTATGATCCCATGAAATATGAATCAAAAGAGGTAAG--CAAGGGGTGT 1000
 DB 907 TTGAGTTGTTATGATCCCATGAAATATGAATCAAAAGAGGTCAAGTGTGTGTGT 966
 QY 1001 GTGCGATTCTT----- 1011
 DB 967 GTGTGATTTCTTTGCAACTTCAAGGTGAGAAAGCTCTTCAACTGACAGGACAGACA 1026
 QY 1012 -----TCTACTGTGCTGACGTGACGCCGCCCTCTTCTTCCAGCAATTAACATTT 1063
 DB 1027 GGTGGCCCTGCTACTGTGCTGACGTGACGCCCTCTTCTTCTTCAATTAACATC 1086
 QY 1064 CAGCAGCTTGAACCTAA--GACTGTGTGACAGGAGGAGTCTCCAGGACAGACGCCAGC 1122
 DB 1087 CAACAGCTTCACTGAACTCACTGCTGTCAAGGACAGGAAAGCTCCATGCACTAGCCAGC 1146
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 DB 1147 AAAGAGCAACACAGAGCTGAAAGAGTCAAGAGAGAGATTAAGTAAAGAAAGT 1206
 QY 1183 GATGAGCTTATCCCAATTTTGGGGGTGAGAACTGTGCTTCTCTGCTGTCAAGCTGTGT 1242
 DB 1207 GATGAGCTTATCCCAATTTTGGGGGTGAGAACTGTGCTTCTCTGCTGTCAAGCTGTGT 1266
 QY 1243 GCTCCTCTATCT 1254

DB 1267 GCTCCTCTATCT 1278

RESULT 4
 US-09-023-655-1060
 ; Sequence 1060, Application US/09023655
 ; Patent No. 6607879
 ; GENERAL INFORMATION:
 ; APPLICANT: Cocks, Benjamin G.
 ; APPLICANT: Susan G. Stuart
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE.
 ; NUMBER OF SEQUENCES: 1508
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3174 PORTER DRIVE
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/023,655
 ; FILING DATE: HEREWITH
 ; CLASSIFICATION:
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Zeller, Karen J.
 ; REGISTRATION NUMBER: 37,071
 ; REFERENCE/DOCKET NUMBER: PA-0001 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 855-0555
 ; TELEFAX: (650) 845-4166
 ; INFORMATION FOR SEQ ID NO: 1060:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1707 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: GENBANK
 ; CLONE: g181345
 ; US-09-023-655-1060
 Query Match 11.3%; Score 142; DB 4; Length 1707;
 Best Local Similarity 93.7%; Pred. No. 4.2e-37;
 Matches 148; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 1097 GGAATGCTCCAGGACAGACAGCCCAAGCAACACAGACACAGCTGAAAGTAAAGTCA 1156
 DB 1 GGGAGGCTCCAGGACAAACAGCCCAAGCAACACAGACACAGCTGAAAGGAAAGCTCACA 60
 QY 1157 GGAACAGTTGAAGAGGCAAGTGGGAGTGAACCTCATCCCAATTTGGGGGTGAAACC 1216
 DB 61 GAACACAGTTGAAGAGGCAAGTGGGAGTGAACCTCATCCCAATTTGGGGGTGAAACC 120
 QY 1217 TGGCTTCTCTGCTGTCAAGCTGTGCTCTCTATCT 1254
 DB 121 TGGCTTCTCTGCTGTCAAGCTGTGCTCTCTATCT 158
 RESULT 5
 US-09-023-655-1405
 ; Sequence 1405, Application US/09023655

```
/ Patent No. 6607879
/ GENERAL INFORMATION:
/ APPLICANT: Cocks, Benjamin G.
/ APPLICANT: Susan G. Stuart
/ APPLICANT: Jeffrey J. Seilhamer
/ TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
/ NUMBER OF SEQUENCES: 1508
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
/ STREET: 3174 PORTER DRIVE
/ CITY: PALO ALTO
/ STATE: CALIFORNIA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/023,655
/ FILING DATE: HEREMITH
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Zeller, Karen J.
/ REGISTRATION NUMBER: 37,071
/ REFERENCE/DOCKET NUMBER: PA-0001 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (650) 855-0555
/ TELEFAX: (650) 845-4166
/ INFORMATION FOR SEQ ID NO: 1405:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1599 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: GENBANK
/ CLONE: g438625
/ US-09-023-655-1405

Query Match          10.2%; Score 128.2; DB 4; Length 1599;
Best Local Similarity 94.3%; Pred. No. 1.9e-32;
Matches 133; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1114 CAGCCGAGCAAAACAAGACAGCTGAAAGTAAGACTCAGAGAGACAGTTGAAAG 1173
DB 2 CAGCCGAGCAAAACAAGACAGCTGAAAGTAAGACTCAGAGAGACAGTTGAAAGAG 61
QY 1174 GCAAGTGGCGATGAGACTCATCCCAAAATTGGCGGTGAAAACCTGGCTTCTCTGGCTGT 1233
DB 62 GAAAGTGGCGATGAGACTCATCCCAAAATTGGCGGTGAAAACCTGGCTTCTCTGGCTGT 121
QY 1234 CAGCTGTGTCTCTCTATCT 1254
DB 122 CAGCTGTGTCTCTCTATCT 142

RESULT 6
US-09-023-655-1062
/ Sequence 1062, Application US/09023655
/ Patent No. 6607879
/ GENERAL INFORMATION:
/ APPLICANT: Cocks, Benjamin G.
/ APPLICANT: Susan G. Stuart
/ APPLICANT: Jeffrey J. Seilhamer
/ TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
/ TITLE OF INVENTION: EXPRESSION
```

```
/ NUMBER OF SEQUENCES: 1508
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
/ STREET: 3174 PORTER DRIVE
/ CITY: PALO ALTO
/ STATE: CALIFORNIA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/023,655
/ FILING DATE: HEREMITH
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Zeller, Karen J.
/ REGISTRATION NUMBER: 37,071
/ REFERENCE/DOCKET NUMBER: PA-0001 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (650) 855-0555
/ TELEFAX: (650) 845-4166
/ INFORMATION FOR SEQ ID NO: 1062:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2059 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: GENBANK
/ CLONE: g181373
/ US-09-023-655-1062

Query Match          9.8%; Score 122.6; DB 4; Length 2059;
Best Local Similarity 85.1%; Pred. No. 1.8e-30;
Matches 137; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1094 GCAGGAGTGTCTCAGAGCAGACAGCCCAAGCAACACACACAGCTGAAAGTAAGACTC 1153
DB 1 GCAGGAAAGCTCCATGCACATAGCCCAAGCAACACACAGCTGAAAGTAAGACTC 60
QY 1154 AGAGGAGACAGTTGAAGAAGGCAAGTGGGATGACCTCATCCCAATTGGGGGTGAA 1213
DB 61 AGAGGAGAGAGATGAAGTGAAGAAAGTATGATGCTCTCATCCAGCTTGGGCATGAA 120
QY 1214 ACCTGGCTTCTCTGGCTGTCACTGAGCTGAGTCTCTATCT 1254
DB 121 ACCTGGCTTCTCTGGCTGTCACTGAGCTGAGTCTCTCTATCT 161

RESULT 7
US-09-583-447A-1
/ Sequence 1, Application US/09583447A
/ Patent No. 6645745
/ GENERAL INFORMATION:
/ APPLICANT: WOJNOWSKI, Leszek
/ APPLICANT: GELNER, Klaus
/ APPLICANT: EISELT, Regina
/ TITLE OF INVENTION: IDENTIFICATION OF A NEW MEMBER OF THE CYTOCHROME P450 3A
/ FILE REFERENCE: 310115.401
/ CURRENT APPLICATION NUMBER: US/09/583,447A
/ NUMBER OF SEQ ID NOS: 45
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1
/ LENGTH: 1659
```



```

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (105)..(1616)
US-09-583-447A-1
```

```

Query Match
Best Local Similarity 76.0%; Pred. No. 1.5e-25; Length 1659;
Matches 133; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
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```

QY 1080 GACTGTGTGACGAGGAGGATGCTCCAGCAGACGCCAGCAAAACAGACACAGC 1139
DB 1 GACCTCTGGGCAAGAAACAAAGCTCTATATGACAGCCAGCAAAAGACAGCAGCAGC 60
QY 1140 TGAATTAAGACTCAGAGGAGACAGTTGAAGAGGCAAGTGGGATGACTATCCCA 1199
DB 61 TGAAGAAAAAATCTCAGAAAGCAGAGCTGAAAAAAGAAACTGGTGAATCTCATTC 120
QY 1200 ATTGGCGGTGAAACCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1254
DB 121 ACTTGCCATGAAACATGAGGTTCTTGTGCTACAGCTGTAATCTCTATAT 175
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RESULT 8

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US-09-144-367-1
; Sequence 1, Application US/09144367
; Patent No. 6432639
; GENERAL INFORMATION:
; APPLICANT: Lichter, Jay
; APPLICANT: Guido, Marco
; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
; FILE REFERENCE: SEQ-12P
; CURRENT APPLICATION NUMBER: US/09/144,367
; CURRENT FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/058,612
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2759
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (70)..(1581)
; OTHER INFORMATION: Human CYP3A4 cDNA reference sequence
US-09-144-367-1
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Query Match
Best Local Similarity 8.2%; Score 102.6; DB 4; Length 2759;
Matches 114; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
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```

QY 1122 CAAACACAGCAGCAGCTGAAAGTAAGTCAAGAGAGACAGTTGAAGAGCAAGTGG 1181
DB 8 CAAAGACACACAGAGCTGAAAGAGACTCAGAGAGAGAGATAAGTAAGAGAAAGTAG 67
QY 1182 CGATGACCTCATCCCAATTGGCGGTGAAAACCTGGCTTCTGCTGCTGCTGCTG 1241
DB 68 TGATGCTCTCATCCAGAGCTGGCCATGAGAACTGGCTTCTGCTGCTGCTGCTGCTG 127
QY 1242 TGCTCTCTATCT 1254
DB 128 TGCTCTCTATCT 140
```

RESULT 9

```

US-09-583-447A-41
; Sequence 41, Application US/09583447A
; Patent No. 6645745
; GENERAL INFORMATION:
; APPLICANT: WOJNOMSKI, Leszek
; APPLICANT: GELINER, Klaus
```

```

; APPLICANT: EISELT, Regina
; TITLE OF INVENTION: IDENTIFICATION OF A NEW MEMBER OF THE CYTOCHROME P450 3A
; TITLE OF INVENTION: (CYP3A) GENE FAMILY: CYP3AX
; FILE REFERENCE: 310115.401
; CURRENT APPLICATION NUMBER: US/09/583,447A
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 105
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-583-447A-41
```

```

Query Match
Best Local Similarity 7.1%; Score 89; DB 4; Length 105;
Matches 95; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
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```

QY 1082 CTGCTGTGAGGAGGAGATGCTCCAGCAGACGCCAGCAAAACAGACACAGCTG 1141
DB 1 CTGCTGTGAGGAGGAGGAGGAGCTCCAGGCAAAAGCCAGCAAAACAGACACAGCTG 60
QY 1142 AAGTAAGACTCAGAGAGACAGTTGAAGAGGCAAGTGGCGATG 1186
DB 61 AAGGAAGACTCAGAGAGACAGTTGAAGAGGAAAGTGGCGATG 105
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RESULT 10

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US-09-583-447A-40
; Sequence 40, Application US/09583447A
; Patent No. 6645745
; GENERAL INFORMATION:
; APPLICANT: WOJNOMSKI, Leszek
; APPLICANT: GELINER, Klaus
; APPLICANT: EISELT, Regina
; TITLE OF INVENTION: IDENTIFICATION OF A NEW MEMBER OF THE CYTOCHROME P450 3A
; FILE REFERENCE: 310115.401
; CURRENT APPLICATION NUMBER: US/09/583,447A
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 106
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-583-447A-40
```

```

Query Match
Best Local Similarity 6.3%; Score 78.8; DB 4; Length 106;
Matches 89; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
```

```

QY 1081 ACTGCTGTGAGGAGGAGATGCTCCAGCAGACGCCAGCAAAACAGACACAGCT 1140
DB 1 ACTGCTGTGAGGAGGAGGAGGAGCTCCAGCAGACGCCAGCAAAACAGACAGCGTGT 60
QY 1141 GAAAGTAAGACTCAGAGAGACAGTTGAAGAGGCAAGTGGCGATG 1186
DB 61 GAAAGTAAGACTCAGAGAGAGATGAAGAGGAAAGTAGTGATG 106
```

RESULT 11

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US-09-583-447A-39
; Sequence 39, Application US/09583447A
; Patent No. 6645745
; GENERAL INFORMATION:
; APPLICANT: WOJNOMSKI, Leszek
; APPLICANT: GELINER, Klaus
; APPLICANT: EISELT, Regina
; TITLE OF INVENTION: IDENTIFICATION OF A NEW MEMBER OF THE CYTOCHROME P450 3A
; FILE REFERENCE: 310115.401
; CURRENT APPLICATION NUMBER: US/09/583,447A
```

;; CURRENT FILING DATE: 2000-05-30
;; NUMBER OF SEQ ID NOS: 45
;; SOFTWARE: Patentin Ver. 2.1
;; SEQ ID NO 39
;; LENGTH: 106
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-583-447A-39

Query Match 6.2%; Score 77.2; DB 4; Length 106;
Best Local Similarity 83.0%; Pred. No. 4.7e-16;
Matches 88; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 1081 ACTGCTGTGACGGGAGGAGTCTCCAGGACAGACCCAGCAACACAGCAGCT 1140
Db 1 ACTGCTGTGACGGGAGGAGTCTCCAGCATTGACCATGAGCCAGCAACACAGCAGCT 60
Qy 1141 GAAGTAGACTCAGAGGACAGTGTGAAGAGCAATGGCGANG 1186
Db 61 GAAGGAAAGACTCAGAGGAGAGATGAAGTGAAGAGTATGATG 106

RESULT 12

US-08-232-463-14/C
; Sequence 14, Application US/08232463
; Patent No. 5670367

;; GENERAL INFORMATION:
;; APPLICANT: DORNER, F.
;; APPLICANT: SCHEIFLINGER, F.
;; APPLICANT: FALKNER, F. G.
;; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
;; NUMBER OF SEQUENCES: 52
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Foley & Lardner
;; STREET: 1800 Diagonal Road, Suite 500
;; CITY: Alexandria
;; STATE: VA
;; COUNTRY: USA
;; ZIP: 22313-0299

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/232.463
;; FILING DATE:
;; CLASSIFICATION: 435

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/07/935.313
;; FILING DATE:

;; APPLICATION NUMBER: EP 91 114 300.6
;; FILING DATE: 26-AUG-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BENT, Stephen A.

;; REGISTRATION NUMBER: 29,768
;; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703)836-9300
;; TELEFAX: (703)683-4109

;; TELEX: 899149
;; INFORMATION FOR SEQ ID NO: 14:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 7218 base pairs

;; TYPE: nucleic acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; IMMEDIATE SOURCE:

;; CLONE: pTZgt-F1s

US-08-232-463-14

Query Match 5.8%; Score 72.6; DB 1; Length 7218;
Best Local Similarity 1.6%; Pred. No. 3.7e-13;

Matches 6; Conservative 240; Mismatches 129; Indels 0; Gaps 0;

Qy 489 GTCACGGTCATGAAGTAATAATACAGACTGTGCCCTTAGGAATCAGCTGTGCT 548
Db 1439 GTACACRR 1380

Qy 549 AAGGAAACAGACACAAACCCACAGGCTGTAGAGAGAAATAGACAATAGAGATG 608
Db 1379 RRR 1320

Qy 609 TGTGAGGGGATAGAGGACACCCAGAGGAAATGTTATCTGTGTGAGAGTTGG 668
Db 1319 RRR 1260

Qy 669 TAAGAAAGACTTAATGAAGGGCTGTGCTGCGCTTGAAGATGTGAGAT 728
Db 1259 RRR 1200

Qy 729 CATTAGGGGACACAGTACCTCCAGGACAGAGGAATGATGTTAAATCTGCACT 788
Db 1199 RRR 1140

Qy 789 TGTGCTGTGAGGATGATTTCAAGTATTCGAATGAGACAGCCATGAGAAAGGG 848
Db 1139 RRR 1080

Qy 849 CAGGTAGAGATAT 863
Db 1079 RRRRRRRRRRRRRAT 1065

RESULT 13
US-08-277-031B-4
; Sequence 4, Application US/08277031B
; Patent No. 6620593

;; GENERAL INFORMATION:
;; APPLICANT: Hayaeshi, Koji
;; APPLICANT: Sakaki, Toshiyuki
;; APPLICANT: Yabusaki, Yoshiyasu
;; APPLICANT: Komai, Koichiro
;; APPLICANT: Kaneko, Hideo
;; APPLICANT: Nakatsuka, Iwao
;; TITLE OF INVENTION: METHOD FOR SAFETY EVALUATION OF
;; TITLE OF INVENTION: CHEMICAL COMPOUND USING RECOMBINANT YEAST EXPRESSING
;; TITLE OF INVENTION: HUMAN CYTOCHROME P450
;; NUMBER OF SEQUENCES: 42
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Birch, Stewart, Kolasch & Birch
;; STREET: P.O. Box 747
;; CITY: Falls Church
;; STATE: Virginia
;; COUNTRY: USA
;; ZIP: 22040-0747

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.5inch, 1.44MB
;; COMPUTER: IBM PC
;; OPERATING SYSTEM: Dos 5.0
;; SOFTWARE: WordPerfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/277.031B
;; FILING DATE: 19-JULY-1994

;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP-201120/1993
;; APPLICATION NUMBER: JP-180246/1993
;; APPLICATION NUMBER: JP-208279/1993
;; FILING DATE: 20-07-1993
;; FILING DATE: 21-07-1993
;; FILING DATE: 30-07-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Raymond C. Stewart
;; REGISTRATION NUMBER: 21,066
;; REFERENCE/DOCKET NUMBER: 20-3530P

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1512
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
;
; US-08-277-031B-4

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Query Match          4.9%; Score 61.4; DB 4; Length 1512;
Best Local Similarity 91.5%; Pred. No. 7.3e-10;
Matches 65; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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```

QY 1184 ATGAACTCATCCCAATTGGCGGTGAAACCTGCTTCTCTGCTGTACAGCTGTG 1243
DB 1 ATGGCTCTCATCCAGACTTGGCCATGGAACCTGCTTCTCTGCTGTACAGCTGTG 60
QY 1244 CTCCTCTACTCT 1254
DB 61 CTCCTCTACTCT 71

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RESULT 14

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; US-09-583-447A-42
; Sequence 42, Application US/09583447A
; Patent No. 6645745
; GENERAL INFORMATION:
; APPLICANT: WOJNOMSKI, Leszek
; APPLICANT: WOJNOMSKI, Klaus
; APPLICANT: GELNER, Regina
; APPLICANT: BISSETT, Regina
; TITLE OF INVENTION: IDENTIFICATION OF A NEW MEMBER OF THE CYTOCHROME P450 3A
; FILE REFERENCE: 310115.401
; CURRENT APPLICATION NUMBER: US/09/583,447A
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 106
; TYPE: DNA
; ORGANISM: Homo sapiens
;
; US-09-583-447A-42

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```

Query Match          4.9%; Score 61.2; DB 4; Length 106;
Best Local Similarity 73.6%; Pred. No. 1.2e-10;
Matches 78; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

```

```

QY 1081 ACTGCTGTGCAAGGCGAGATGCTCCAGCAGACAGCCCAAGCAACAGACACAGCT 1140
DB 1 ACCTCTGGGCAAGAAACAAAGCTCTATATGCAAGCCCAAGCAAGACAGACACAGCT 60
QY 1141 GAAAGTAAGACTCAGAGAGAGACAGTGAAGAGCAAGTGGCGATG 1186
DB 61 GAAAGTAAGACTCAGAGAGAGACAGTGAAGAGCAAGTGGCGATG 106

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RESULT 15

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; US-09-172-108-12
; Sequence 12, Application US/09172108
; Patent No. 6160104
; GENERAL INFORMATION:
; APPLICANT: Cunningham, Mary Jane
; APPLICANT: Zweigler, Gary B.
; APPLICANT: Panzer, Scott R.
; APPLICANT: Seilhammer, Jeffrey J.
; TITLE OF INVENTION: MARKERS FOR PEROXISOMAL PROLIFERATORS
; FILE REFERENCE: PA-0012 US
; CURRENT APPLICATION NUMBER: US/09/172,108
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 56

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; SOFTWARE: PERL Program
; SEQ ID NO 12
; LENGTH: 243
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 33
; OTHER INFORMATION: a or g or c or t, unknown, or other
;
; OTHER INFORMATION: 700141708H1
;
; US-09-172-108-12

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Query Match          4.1%; Score 51; DB 3; Length 243;
Best Local Similarity 69.7%; Pred. No. 6.3e-07;
Matches 83; Conservative 0; Mismatches 35; Indels 1; Gaps 1;

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QY 1134 CACAGCTGAAGTAAGACTCAGAGAGACAGTTGAGA-AGGCAAGTGCGATGACCTC 1192
DB 35 CCCAGCTAGAGGAGACACACAGAGAGTAATTGCTGACAGACCTGACAGGAGTGAAGCTG 94
QY 1193 ATCCCAATTGGCGGCTGGAACCTGCTTCTCTGCTGTGCTGCTGCTCTCTCTA 1251
DB 95 CTTGAGCTCTCAGACTGGAACCTGGGCTCTCTGCGAGTGTCTCTGCTCTCTCTA 153

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Job time : 106.779 secs

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OM nucleic - nucleic search, using sw model

Run on: January 26, 2005, 17:54:48 : Search time 628.441 Seconds
(without alignments)
11465.419 Million cell updates/sec

Title: SEQ4-1037G
Perfect score: 1254
Sequence: 1 GGCACACAAAGAGACATGTC.....AGCCGTGTCCTCCTCATCT 1254

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

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- 2: /cgn2_6/prodata/1/pubpna/PCT_NEW_PUB.seq:*
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- 9: /cgn2_6/prodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/prodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/prodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/prodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/prodata/1/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/prodata/1/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq:*
- 19: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1252.4	99.9	1254	16	US-10-085-612-4
2	664	53.0	8776	16	US-10-257-166-149
3	567.4	45.2	8776	16	US-10-257-166-150
4	498.8	39.8	1345	14	US-10-146-575-3
5	498.8	39.8	1345	14	US-10-085-612-3
6	498.4	39.7	1345	10	US-09-943-115A-1
7	457.2	36.5	13035	15	US-10-121-960C-14
8	434.6	34.7	15185	15	US-10-121-960C-17
9	396.4	31.6	11186	9	US-09-957-997-1
10	387.2	30.9	1012	9	US-09-957-997-4
11	253.4	20.2	8943	16	US-10-257-166-47
12	222.8	17.8	8943	16	US-10-257-166-48

13	142	11.3	1707	9	US-09-880-107-2114	Sequence 2114, Ap
14	142	11.3	1707	16	US-10-641-643-1060	Sequence 1060, Ap
15	141	11.2	384	9	US-09-925-297-24	Sequence 24, Appl
16	135.6	10.8	2768	15	US-10-268-827-14	Sequence 14, Appl
17	135.6	10.8	2768	15	US-10-388-360-297	Sequence 297, Appl
18	135.6	10.8	2768	15	US-10-388-360-353	Sequence 363, Appl
19	128.2	10.2	1599	16	US-10-641-643-1405	Sequence 1405, Ap
20	126.6	10.1	1595	9	US-09-880-107-3816	Sequence 3816, Ap
21	123.8	9.9	2059	15	US-10-106-698-1724	Sequence 1724, Ap
22	122.6	9.8	2059	16	US-10-641-644-1062	Sequence 1062, Ap
23	107.8	8.6	1659	13	US-10-007-814-1	Sequence 1, Appl
24	107.6	8.6	1915	16	US-10-112-944-188	Sequence 188, Appl
25	103.8	8.3	2849	9	US-09-880-107-2110	Sequence 2110, Ap
26	102.6	8.2	2759	13	US-10-146-575-1	Sequence 1, Appl
27	96.4	7.7	489	14	US-10-027-632-277590	Sequence 277590,
28	96.4	7.7	489	15	US-10-027-632-277590	Sequence 277590,
29	94.8	7.6	2011	9	US-09-880-107-1586	Sequence 1586, Ap
30	89	7.1	105	13	US-10-007-814-41	Sequence 41, Appl
31	78.8	6.3	106	13	US-10-007-814-40	Sequence 40, Appl
32	77.2	6.2	106	13	US-10-007-814-39	Sequence 39, Appl
33	72.8	5.8	240	9	US-09-960-352-15077	Sequence 15077, A
34	72.8	5.8	380	9	US-09-960-352-15107	Sequence 15107, A
35	72.8	5.8	411	9	US-09-960-352-4176	Sequence 4176, Ap
36	72.8	5.8	418	9	US-09-960-352-4657	Sequence 4657, Ap
37	72.8	5.8	422	9	US-09-960-352-6070	Sequence 6070, Ap
38	72.8	5.8	430	9	US-09-960-352-8232	Sequence 8232, Ap
39	71.4	5.7	347	9	US-09-960-352-3467	Sequence 3467, Ap
40	71.4	5.7	442	9	US-09-960-352-1762	Sequence 1762, Ap
41	71.2	5.7	339	9	US-09-960-352-8257	Sequence 8257, Ap
42	70.2	5.6	207	9	US-09-960-352-9871	Sequence 9871, Ap
43	70.2	5.6	404	9	US-09-960-352-7510	Sequence 7510, Ap
44	69.6	5.6	209	9	US-09-960-352-9181	Sequence 9181, Ap
45	66.4	5.3	322	9	US-09-960-352-6312	Sequence 6312, Ap

ALIGNMENTS

RESULT 1
US-10-085-612-4
: Sequence 4, Application US/10085612
: Publication No. US2003096251A1
: GENERAL INFORMATION:
: APPLICANT: Guida, Marco
: APPLICANT: Hall, Jeff
: APPLICANT: Petros, William
: APPLICANT: Vredenburg, James
: APPLICANT: Colvin, Oliver
: APPLICANT: Marks, Jeffrey
: TITLE OF INVENTION: Methods for Evaluating the Ability to Metabolize Pharmaceuticals
: FILE REFERENCE: 4389-5-C1
: CURRENT APPLICATION NUMBER: US/10/085,612
: CURRENT FILING DATE: 2002-02-26
: PRIOR APPLICATION NUMBER: 09/144,367
: PRIOR FILING DATE: 1998-08-31
: PRIOR APPLICATION NUMBER: 60/271,630
: PRIOR FILING DATE: 2001-02-26
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 4
: LENGTH: 1254
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-10-085-612-4

Query Match 99.9%; Score 1252.4; DB 14; Length 1254;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1253; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCACACAAAGAGACATGTCATGTTCTACTTATTTGTGGATCTACAAATCAAAACAT 60
DB 1 GGCACACAAAGAGACATGTCATGTTCTACTTATTTGTGGATCTACAAATCAAAACAT 60

QY 61 TGAGCTAATGTCGGGCTTATGTCATTTTGTACCCCTAAGTACAGGAGACAGCCATTA 120
 DB 61 TGAGCTAATGTCGGGCTTATGTCATTTTGTACCCCTAAGTACAGGAGACAGCCATTA 120
 QY 121 GAATACATGATGTAATGCTTTATACAGGAATGAATAGGTAGAGAGCAGAGGTGTTGG 180
 DB 121 GAATACATGATGTAATGCTTTATACAGGAATGAATAGGTAGAGAGCAGAGGTGTTGG 180
 QY 181 TGTCTCTGATACATAGTATCTTCTTGACACATTCAGTACAACTCTCAACAGGTAAGT 240
 DB 181 TGTCTCTCTATACATAGTATCTTCTTGACACATTCAGTACAACTCTCAACAGGTAAGT 240
 QY 241 CTCTTCATGATGTAATGCTTCTTGAGAAATTAAGTGGAGAAATGCTTCAATTAATTTTC 300
 DB 241 CTCTTCATGATGTAATGCTTCTTGAGAAATTAAGTGGAGAAATGCTTCAATTAATTTTC 300
 QY 301 CTCTTCAGAAACAAAGCCAAATTCATGTTGGGAAACAGTCTGGCTGCATCTGAGCCCC 360
 DB 301 CTCTTCAGAAACAAAGCCAAATTCATGTTGGGAAACAGTCTGGCTGCATCTGAGCCCC 360
 QY 361 AAGCAACATTAATGCTATTCATCAACAGACTCAGAGGGGATGACACAGAGGGCCC 420
 DB 361 AAGCAACATTAATGCTATTCATCAACAGACTCAGAGGGGATGACACAGAGGGCCC 420
 QY 421 AGCAATCTCAACCAAGTCACTCCACCAATTTCTGTCACCCACCATGTGTACATAC 480
 DB 421 AGCAATCTCAACCAAGTCACTCCACCAATTTCTGTCACCCACCATGTGTACATAC 480
 QY 481 CTTGCTAAGGTCACAGGTCATGAAAGTAAATTAATCCAGCTGCTGCTTGAAGAACTCA 540
 DB 481 CTTGCTAAGGTCACAGGTCATGAAAGTAAATTAATCCAGCTGCTGCTTGAAGAACTCA 540
 QY 541 CCTCTGTAAGGAAACAGGACACAGAAACCAAGGGGTGTAGAGAGAAATAGACAA 600
 DB 541 CCTCTGTAAGGAAACAGGACACAGAAACCAAGGGGTGTAGAGAGAAATAGACAA 600
 QY 601 TAGGACTGTGTAGAGGGGATGAGAGCACCAGAGAGAAATGTTACATCTGTGTAG 660
 DB 601 TAGGACTGTGTAGAGGGGATGAGAGCACCAGAGAGAAATGTTACATCTGTGTAG 660
 QY 661 GAGGTGTGTAGAAANAATTTAATGAAAGGGGTCTGTGCTGGCTTGAAGAGTGT 720
 DB 661 GAGGTGTGTAGAAANAATTTAATGAAAGGGGTCTGTGCTGGCTTGAAGAGTGT 720
 QY 721 GTAGAGTCACTTAGAGGGGACAAAGTACCTCCAGGACAGAGGAATGCAAGGTAAAGA 780
 DB 721 GTAGAGTCACTTAGAGGGGACAAAGTACCTCCAGGACAGAGGAATGCAAGGTAAAGA 780
 QY 781 TCTGCAATGTGTGCTGTGGGGATGATTTCAAGTATTTGGAATGAAACAGCCATGGA 840
 DB 781 TCTGCAATGTGTGCTGTGGGGATGATTTCAAGTATTTGGAATGAAACAGCCATGGA 840
 QY 841 AACAAGGGGAGGTGAGAGGATTTTAAGAGGCTTCAAGCCATGCTCCACTCAAGTTTC 900
 DB 841 AACAAGGGGAGGTGAGAGGATTTTAAGAGGCTTCAAGCCATGCTCCACTCAAGTTTC 900
 QY 901 TGATTAAGAACTCAGGTTCCGTGACCTCCATGATTAATGATTAAGTTGTTATGATTC 960
 DB 901 TGATTAAGAACTCAGGTTCCGTGACCTCCATGATTAATGATTAAGTTGTTATGATTC 960
 QY 961 CCATAGAAATGAACTCAAGAGGTGAGCAAGAGGGGTGTGTGAGATTTCTTGTACTGG 1020
 DB 961 CCATAGAAATGAACTCAAGAGGTGAGCAAGAGGGGTGTGTGAGATTTCTTGTACTGG 1020
 QY 1021 CTGCAAGTGAAGCCCGCTCTCTTCTCCAGACATTAACATTTTCAGAGCTTGAAGCTTAAG 1080
 DB 1021 CTGCAAGTGAAGCCCGCTCTCTTCTCCAGACATTAACATTTTCAGAGCTTGAAGCTTAAG 1080
 QY 1081 ACTGCTGTGAGAGGACAGAGTGTCCAGGACAGAGCCAGCAAAACAGACAGACAGCT 1140
 DB 1081 ACTGCTGTGAGAGGACAGAGTGTCCAGGACAGAGCCAGCAAAACAGACAGACAGCT 1140

QY 1141 GAAAGTAAAGCTAGAGGAGACAGTGAAGAGGCAAGTGGCATGAGACTCATCCCAA 1200
 DB 1141 GAAAGTAAAGCTAGAGGAGACAGTGAAGAGGCAAGTGGCATGAGACTCATCCCAA 1200
 QY 1201 TTGGGGGAGGAGAAACCGGCTTCTCGGCTGTGACGCTGTGCTGCTATCT 1254
 DB 1201 TTGGGGGAGGAGAAACCGGCTTCTCGGCTGTGACGCTGTGCTGCTATCT 1254
 RESULT 2
 US-10-257-166-149
 ; Sequence 149, Application US/10257166
 ; Publication No. US2004023230A1
 ; GENERAL INFORMATION:
 ; APPLICANT: OLEK, Alexander
 ; APPLICANT: PIEPENBROCK, Christian
 ; APPLICANT: BERLIN, Kurt
 ; TITLE OF INVENTION: Method and Nucleic Acid for Analysing the Methylation of
 ; FILE REFERENCE: 5013.1011
 ; CURRENT APPLICATION NUMBER: US/10/257,166
 ; CURRENT FILING DATE: 2002-10-07
 ; PRIOR APPLICATION NUMBER: PCT/EP01/07470
 ; DE 10032529.7
 ; DE 10043826.1
 ; PRIOR FILING DATE: 2001-06-29
 ; 2000-06-30
 ; 2000-09-01
 ; NUMBER OF SEQ ID NOS: 178
 ; SEQ ID NO 149
 ; LENGTH: 8776
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
 US-10-257-166-149
 Query Match 53.0%; Score 664; DB 16; Length 8776;
 Best Similarity 73.4%; Pred. No. 9e-207;
 Matches 919; Conservative 0; Mismatches 320; Indels 13; Gaps 5;
 QY 4 ACAAGAGAGACATTCATGTTCTCTCACTTATTTGSGGATCTCAATCAATCAATCAATG 63
 DB 3919 AGAAATATGATATATGTTATGTTTATATATATTTGAGATTTTAAATTAATTAATG 3978
 QY 64 GCTAATGCTGGGCTTAACTTATGTAACCTTAAGTACAGGAGACAGCCATTAAGA 123
 DB 3979 GTTAATGTTGGTTTAAAGTATGTTGTA-TTTAAGTATGGGAGTATAGTTTAA 4037
 QY 124 TACATATGATGCTTTAATACAGAAATGATATGTAAGAGGACAGAGGTGTTGGTGT 183
 DB 4038 TATATATGATGATTTTAAATATGATGATGATGATGATGATGATGATGATGATG 4097
 QY 184 TCTTCGATACATAGTATCTCTCTGACATTCATCAATCAATCAATCAATGATGTC 243
 DB 4098 TTTTGTATATATATATATATTTTATATGATATGATATATATTTTAAATGATGAT 4157
 QY 244 TTCAATG-TATGTTAACCCTCGAGAAATTAAGTGGCAACATGCTTCTATTAATTTTCT 302
 DB 4158 TTTATGTATATGTTATTTATGAGAAATTAAGTGTGAATTAATTTTATTTT 4217
 QY 303 TTGCAAGACAGCAATTCATTAAGTGTGGGAAACAGTGTGCTGCTCATGAGCCCAA 362
 DB 4218 TTGTAGAAATTAAGTATTAATTTATTAAGTGGATATATG-TGGTGTATTTGAGTTTAA 4276
 QY 363 GCAACATTAATGCTATGCTATCAACACAGACTCAAGAGGAGAGACACAGGGGCCCG 482
 DB 4277 GTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4330
 QY 423 CAATCTCACCAAGTCACTCCACCAACATTTCTGTGACCCACCAATGATAGTACCC 482
 DB 4331 TAAATTTATTAAGATTAATTTTATTAATTTTGTGATTTATTTATGATATAGTATTT 4390

Oy	483	TGCTAAGGCTCCAGGGTCATGAAGTAATAATACCGACACTGTCGCTTGTAGGAACTCACC	542
Db	4391	TGTTAGGAATTTAGGGTTATAGAACTAATAATATTTGATTTGTCTTTTGGAGCTTTATT	4450
Oy	543	TCTGCTAAGGAAACAGGCA CAGAAACCCACAAGGGTGTAGAGAAATAGACAAATA	602
Db	4451	TTTCTTAAGGGAAATAGGTATAGAAATTTATTAATGGTGTAGAGAAAGAGATATA	4510
Oy	603	GGACTGTGTAGGGGGATAGAGAGCCACCCAGAGAGAAATGGTTACATCTGTGTAGGA	662
Db	4511	GGATTTGTGTGAGGGGATAGAGAGTATTTAGAGAGAGAAATGGTTATATTTGTGTAGGA	4570
Oy	663	GGTTGTAGAGAAAGACTTTAATATGAAGGGGCTCTGCTGGGCTCCAGAGATGCT	722
Db	4571	GGTTGTAGAGAAATTTATAGTAGAAAGGGGTTTGTGTTGGTTGGAGAGATACGT	4630
Oy	723	AGAGATCATCTAGGGGGCACAAAGTACACTCCAGGACAGAGGAATTCATGCTAAAGATC	782
Db	4631	AGGAGTTATTTAGAGGGTTATAGATATTTTAGGTAGAGGAAATTTCTGTGGTAAGATG	4690
Oy	783	TGCAGTTGTGGCTTTGTGGGATGGATTTCAATATCTGSAATGAAGAACCCATGAA	842
Db	4691	TGTAGTGTGGTTGTGAGATGGAATTTATATTTATTAAGAAAGATGATTAAG---	4747
Oy	843	CAAGGCAAGTGAAGAGATATTTAAGAGGCTTCATGCAATGGCTCCACTCAGTTCTG	902
Db	4748	-AGGGGTAGTGAAGAGAGGGTTAATGATTTATATGTTAATGTTTATTTGAGTTTTG	4806
Oy	903	ATAAGAACTCAGGTTCCGTGACACTCCTGATTAACATGATTAAGTTGTTATGATCCCC	962
Db	4807	ATAAGAAATTTAGAATTTTGTGATTTTTCGATTAATATGATTAAGTTTATATGATTTTTT	4866
Oy	963	ATAGAATATGAATCAAAAGAGATPAAGCAAAAGGGGTGTGCGATTTCTTTGCTACTGAGCT	1022
Db	4867	ATAGAATATGAATTTAATAAGAGGTTAGTAATAAGGGGTGTGCGATTTTGTATATGGTT	4926
Oy	1023	GCAGCTGACAGCCCCCTCTCTCTCCAGCACAATAAACATTTACAGCAGCTTGACTTAAGC	1082
Db	4927	GTAATTTATGATTTTGTTTTATTTTATTAATAATTTTATGATTTGTTGTTGAAGAT	4986
Oy	1083	TGCTGTACAGGGCAGGAGATGCTCCAGGCACAGCCAGCAACACAGACACAGCTGA	1142
Db	4987	TGTTGTATAGGATAGGAAAGTTTATAGTAATATGTTTAGTAATAGTATTTAGTTTA	5046
Oy	1143	AAGTAAAGCTCAGAGAGACATTTGAAGAAAGCAGAGTGGCGATGAGACTCATCCCAATT	1202
Db	5047	AAGGAATATTTATAGATATATAGTTGAAGAAAGGAAGTGGGATGAGATTTATATTTAAATT	5106
Oy	1203	TGCGCGGTGAACCTGGCTTCTCCTGGCTGTCAAGCTGTGCTCTCTATCT	1254
Db	5107	TGCGCGGTGAACCTGGCTTCTCCTGGCTGTGCTCTCTATCT	5158

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; SEQ ID NO 150
; LENGTH: 8776
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-257-166-150

Query Match      45.2%; Score 567.4; DB 16; Length 8776;
Best Local Similarity 68.6%; Pred. No. 6.2e-175;
Matches 859; Conservative 0; Mismatches 381; Indels 13; Gaps 5;

QY      3  CACACAAAGAGACATGTGCATGTCCTCACTTATTTGTGGAGCTCAATCAATCAAACAATG 62
Db      4859 CAAACACCAATATTTACAAATCTCACATATCTATATAATCTCAAAATCAAAACAACTA 48000

QY      63  AGCTAATGTCTGGGCTTATGTCAATTTTGTACCTTAAGTACAGGAGACAGCCATTAGA 122
Db      4799 AACCTATATCTAAACCTTAATCAATATATATACCC-AAATCTAATAAACACAACTTTTAA 47411

QY      123  ATACATGATGAATGCTTTAATACAGGAATGAATGGTGAGAGCAAGGGTGTTGGTG 182
Db      4740 ATACATCATTAATCTTTAATACAAAAATAATTAATAAAAAACAAACTTAATTAATA 46811

QY      183  TTCTTCGATCATATAGTATCTTCCCTTGACATTCAGATGCAACCTCAACAGTAAGCT 242
Db      4680 TTCTTCATATACAAATATCTTCTTAAACAAATTCATACAACTCTCAACAAATTAATCT 46211

QY      243  CTTCAT-CTATGTACCTCTGAGGAATTAAGTGGCAGAACATGCTCTTATATTTTCC 301
Db      4620 CTTCATATATATTTACCTTATATAAAATTAATAACAAACATTAATTTCTATATTTTCC 45611

QY      302  TTTCGAGAACAGACCAATTCATTAAGTTGGGAAACAGTGTGCTGATCTGAGCCCA 361
Db      4560 TTTCACAAACAAACCAACTTTATTAATTAACAAAT-ATACTCATTTAATATCCCA 45021

QY      362  AGCAACCTTATGTCTATTTGCTATACACACAGCTCAGAGGGAGTACACAGGGGGCCA 421
Db      4501 AACCAACCTTATCTATTAATCTATACCAACCAAAATCAAAAAATAAAAAAC-----GCCCA 44481

QY      422  GCAATCTCACCAAGTCACTCCACCAACATTTCTGGTCAACCCACATGTGTACATGAC 481
Db      4447 ACAATCTCACCCAAAACAACTCCACCAACATTTCTTAATTAACCAACATATTAACATAC 43881

QY      482  CTGCTAGGGTCCAGGGTCAATGAATTAATATACAGACTGTGCTCCCTTGAGAACTCAC 541
Db      4387 CTACTCAAAAACCAAAATCATATAAATTAATTAATACAACTATACCTTAATAAAATCTAC 43281

QY      542  CTCTGCTTAGGGAAACAGGCACAGAAACCCAGAGGGTGTATGAGAGGAATAGACAAAT 601
Db      4327 CTCTACTAAAAAACAACAACTAAAAAATTAACAATTAATTAATAAAAAAATAAAAAACAAAT 42681

QY      602  AGGACTGTGTAGGGGGATTAGAGAGCAACCCAGAGAGGAATGTGTATCATGTGTGAG 661
Db      4267 AAAACTATATATAAAAAATTAATAAAACCCCAAAAAAATAAATTAATTCATTTATATATAA 42081

QY      662  AGTTGTATAGGAAGAAGCTTATATAGAGGGGTCTGTCTGGCTGGGCTTGCAAGATGTG 721
Db      4207 AAATTAATATAAAAAAATTTTAACAAAAAATTTATCTAATCTTAACCTTAATAAAAAATACG 41481

QY      722  TAGAGTCACTTAGAGGGGACACAGTCACTCCAGGCAGAGGAATTGCAATGGTAAAGAT 781
Db      4147 TAAAAATCATCTAAAAAACAACAAATTAACCTCAAAACAAAAAATTTTGTAAATTAATAAT 40881

QY      782  CTGCACTTTGGCTTGTGGGATAGATTTTCAAGATTTCTGGAATGAAGAGCAGCATGAA 841
Db      4087 ATATTAATATATCTTAATAAATAATTAATTTCAATTAATCTTAATAATAAACAACATTAATA 40281

QY      842  ACAAGGCGAGGTGAGAGATATTTAAGAGGCTTCATGCGCATGTGCTCACTTCAGTTTCT 901
Db      4027 AAA-----CAATTAATAAAAAAATTAATTAATTTCAATCAATTAATCTCACTTAATTTCT 39721

QY      902  GATAAGAACTCAGGTTCCGTGGACTCCCTGATTAATACTGAATTAAGTTTATGATTC 961

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Best Local Similarity 77.7%; Pred. No. 8,4e-153; Matches 709; Conservative 1; Mismatches 128; Indels 74; Gaps 6;

QY 402 GGATGACACAGAGGGCCCGAGCATCTCACCCAAAGTAACTCCACCAATTTCTGTCA 461
DB 382 GGATGACATAGACAGGCGCCAGCAATCTCAGCTAAAGTAACTCCACCGCTTTCTAATTG 441
QY 462 CCACCATGTGTACAGTACCTGCTAGAGGTCCAGGGTCAATGAAGTAATATATACAGAC 521
DB 442 CCACCTGTGTACAGACCTCTGTAGAGACCAAGACCAATGACAGGAAATAGACTAGAC 501
QY 522 TGTGCTTGTAGAGAACTCAGCTCTGTAGAGAAACAGGACCAAGAAACCAAGGGTGG 581
DB 502 TATGCCCTTGTAGAGGCTCAGCTCTGTAGAGAAACAGGGGTGAAA--CACATGTGG 559
QY 582 TAGAGAGAAATATGACATATGACATGTGTAGAGGGGATATGAGGACCCAGAGAGAA 641
DB 560 TAAAGAGAAAGAGCAATATGATGATGATGATGATGATGATGATGATGATGATGATG 619
QY 642 ATGGTTACATCTGTGTAGAGAGGTGTGTAGAGAAAGCTTTAATATGAAAGGGTCTGTG 701
DB 620 ATGGTTACATCTGTGTAGAGAGGTGTGTAGAGAAAGCTTTAATATGAAAG--GGCTGTGTG 678
QY 702 GCTGGCTTGTAGAGATGTGTAGAGATCATCTAGAGGGGCAAAAGTACATCTCAGGACAG 761
DB 679 TCTGGCTTGTAGAGATGTGTAGAGATCTCTAGAGGGGCAAGGACATCTCAG-- 732
QY 762 GGAATTCATGTGTAAAGATCTGATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 821
DB 733 -----GCATAGGTAAAGATCTGTAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 786
QY 822 GAATGAG 881
DB 787 GAATGAG 846
QY 882 ATGGCTTCACTG 941
DB 847 ATGGCTTCACTG 906
QY 942 TTAAGTTGTTATGATTTCCCATATGAAATATGAACTCAAGAGAGTAA--CAAGGGGTGT 1000
DB 907 TTAAGTTGTTATGATTTCCCATATGAAATATGAACTCAAGAGAGTCAAGTGTGTGTGT 966
QY 1001 GTGCGATTTCTT----- 1011
DB 967 GTGCGATTTCTTGTGCAACTTCCAAAGGTGAGAGAGCTTCTTCAACTGACGAGAGACA 1026
QY 1012 -----TGTACTGTGCTGACGCTGAGCCCGCTCTCTTCTCAGACATATTAACATTT 1063
DB 1027 GTGCGCTTCTACTGTGCTGACGCTGAGCCCGCTCTCTTCTCAGACATATTAACATTC 1086
QY 1064 CAGCAGCTTGAACCTTA--GACTGCTGTGACAGGGCAGGAGTGTCTCAGGACAGACCCAGC 1122
DB 1087 CAGCAGCTTGAACCTTAACCTGTGTGTGACAGGGCAGGAGTGTCTCAGTCAATATGACCAGC 1146
QY 1123 AAACAACAGACACAGCTGAAGTAAGTAAGTCAAGAGAGACAGTGAAGAGAGAGAGAGG 1182
DB 1147 AAAGAGAGACACAGAGCTGAAGTAAGTAAGTCAAGAGAGAGAGAGTAAGTAAGAGAGAG 1206
QY 1183 GATGACCTGATCCCAATTTGTGCGGTGAGAACTGTGCTTCTCTGTGCTGTCAAGCTGTG 1242
DB 1207 GATGCGCTCTATCCCAACTTGTGCGCATGAGAACTGTGCTTCTCTGTGCTGTCAAGCTGTG 1266
QY 1243 GCTGCTCTATCT 1254
DB 1267 GCTGCTCTATCT 1278

RESULT 6
US-09-943-115A-1
; Sequence 1, Application US/09943115A
; Publication No. US20030017469A1
; GENERAL INFORMATION:

APPLICANT: SEQUENOM, Inc.
APPLICANT: Risinger, Carl
APPLICANT: Anderson, Maria
APPLICANT: Lewander, Tommy
APPLICANT: Olafsson, Erik
TITLE OF INVENTION: DETECTION OF CYP3A4 AND CYP2C9
FILE REFERENCE: 52459-20021.00
CURRENT APPLICATION NUMBER: US/09/943,115A
CURRENT FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: UK 0021286.0
NUMBER OF SEQ ID NOS: 73
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1345
TYPE: DNA
ORGANISM: Homo sapiens
US-09-943-115A-1

Query Match 39.7%; Score 498.4; DB 10; Length 1345;
Best Local Similarity 77.6%; Pred. No. 1.1e-152; Matches 708; Conservative 2; Mismatches 128; Indels 74; Gaps 6;

QY 402 GGATGACACAGAGGGCCCGAGCATCTCACCCAAAGTAACTCCACCAATTTCTGTCA 461
DB 382 GGATGACATAGACAGGCGCCAGCAATCTCAGCTAAAGTAACTCCACCGCTTTCTAATTG 441
QY 462 CCACCATGTGTACAGTACCTGCTAGAGGTCCAGGGTCAATGAAGTAATATATACAGAC 521
DB 442 CCACCTGTGTACAGACCTCTGTAGAGACCAAGACCAATGACAGGAAATAGACTAGAC 501
QY 522 TGTGCTTGTAGAGAACTCAGCTCTGTAGAGAAACAGGACCAAGAAACCAAGGGTGG 581
DB 502 TATGCCCTTGTAGAGGCTCAGCTCTGTAGAGAAACAGGGGTGAAA--CACATGTGG 559
QY 582 TAGAGAGAAATATGACATATGACATGTGTAGAGGGGATATGAGGACCCAGAGAGAA 641
DB 560 TAAAGAGAAAGAGCAATATGATGATGATGATGATGATGATGATGATGATGATGATG 619
QY 642 ATGGTTACATCTGTGTAGAGAGGTGTGTAGAGAAAGCTTTAATATGAAAGGGTCTGTG 701
DB 620 ATGGTTACATCTGTGTAGAGAGGTGTGTAGAGAAAGCTTTAATATGAAAG--GGCTGTGTG 678
QY 702 GCTGGCTTGTAGAGATGTGTAGAGATCATCTAGAGGGGCAAAAGTACATCTCAGGACAG 761
DB 679 TCTGGCTTGTAGAGATGTGTAGAGATCTCTAGAGGGGCAAGGACATCTCAG-- 732
QY 762 GGAATTCATGTGTAAAGATCTGATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 821
DB 733 -----GCATAGGTAAAGATCTGTAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 786
QY 822 GAATGAG 881
DB 787 GAATGAG 846
QY 882 ATGGCTTCACTG 941
DB 847 ATGGCTTCACTG 906
QY 942 TTAAGTTGTTATGATTTCCCATATGAAATATGAACTCAAGAGAGTAA--CAAGGGGTGT 1000
DB 907 TTAAGTTGTTATGATTTCCCATATGAAATATGAACTCAAGAGAGTCAAGTGTGTGTGT 966
QY 1001 GTGCGATTTCTT----- 1011
DB 967 GTGCGATTTCTTGTGCAACTTCCAAAGGTGAGAGAGCTTCTTCAACTGACGAGAGACA 1026
QY 1012 -----TGTACTGTGCTGACGCTGAGCCCGCTCTCTTCTCAGACATATTAACATTT 1063
DB 1027 GTGCGCTTCTACTGTGCTGACGCTGAGCCCGCTCTCTTCTCAGACATATTAACATTC 1086
QY 1064 CAGCAGCTTGAACCTTA--GACTGCTGTGACAGGGCAGGAGTGTCTCAGGACAGACCCAGC 1122

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Db 1087 CAACAGCTCACTGAATCAGCTGTGTGAGGCGAGGAAGCTTCATGCATACCCAGC 1146
Qy 1123 AACCAACAGCAGAGCTGAAAGTAAGTCAAGAGAGACAGTTGAAGAGGACGTGGC 1182
Db 1147 AAGAGCAACAGAGCTGAAAGAAACATCAGAGAGAGAGATTAAGTAAAGTAAGT 1206
Qy 1183 GATGACCTCATCCCAATTTGGCGGTGAAACCTGCTTCTCTGCTGTCAAGCTGGT 1242
Db 1207 GATGCTCTATCCCAAGCTTGGCCATGAAACCTGCTTCTCTGCTGTCAAGCTGGT 1266
Qy 1243 GCTCCTCTATCT 1254
Db 1267 GCTCCTCTATCT 1278
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RESULT 7

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US-10-121-960C-14
; Sequence 14, Application US/10121960C
; Publication No. US20030145341A1
; GENERAL INFORMATION:
; APPLICANT: ZHANG, Weisheng
; APPLICANT: CONTAG, Pamela
; APPLICANT: PURCHIO, Anthony
; APPLICANT: HASHIMA, Sandy
; APPLICANT: MA, Shirley
; APPLICANT: NAMOTKA, Kevin
; TITLE OF INVENTION: ISOLATION AND IDENTIFICATION OF MOUSE AND HUMAN
; TITLE OF INVENTION: TRANSCRIPTION CONTROL ELEMENTS ASSOCIATED WITH
; TITLE OF INVENTION: CYTOCHROME EXPRESSION
; FILE REFERENCE: 9400-0014 / PXE-014.US
; CURRENT APPLICATION NUMBER: US/10121,960C
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 13035
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human CYP3A4 gene locus
US-10-121-960C-14
```

```
Query Match 36.5%; Score 457.2; DB 15; Length 13035;
Best Local Similarity 77.1%; Pred. No. 1.6e-138;
Matches 665; Conservative 0; Mismatches 123; Indels 74; Gaps 6;

Qy 384 TCACCAAGACTCAGAGGATGACACAGAGGCGCCAGCAATCTCAACCAAGTCACTC 443
Db 12189 TCACCAAGAAAGTCAGAGGATGACATGACAGAGGCCAGCAATCTCAAGTCACTC 12248
Qy 444 CACCAACATTTCTGTCACCAACCATGTGTACAGTACCTGCTAGGGTCCAGGGTCACTGA 503
Db 12249 CACCAAGCTTTCTGTCACCAACCATGTGTGTACAGTACCTGCTAGGGTCCAGGGTCACTGA 12308
Qy 504 AAGTAATTAATACCAAGCTGTGCTTGAAGAACTCACTTCTGCTAAGGAAACAGGCAC 563
Db 12309 CAGGGAATTAAGACTAGCTATGCTTGAAGAGCTCACTTCTGCTAAGGAAACAGGCCT 12368
Qy 564 AGAAACCAAGAGGTGTGAGAGAAATAGCAATAGCACTGTGTAGGGGGAATGG 623
Db 12369 GGAAG--CACAATGTGTGTAAAGAGAAAGCAATAGATTGCAAGAGGGGATGA 12426
Qy 624 AGGACCCAGAGAGAAATGTGTATCATCTGTGTGAGAGAGTTGGTAAAGAAACTTTA 683
Db 12427 AGGTGCCAAGGAGAAATGTGTATCATCTGTGTGAGAGAGTTGGTAAAGAAACTTTA 12486
Qy 684 ATAGAGAGGCTGTGTGTGCTGGCTGCTGCAAGATGTGTAGAGTCACTTAAGGGGACA 743
Db 12487 AGAGAA--GGCTGTGTGTGTGGGTTTGAAGATGTGTAGAGTCTTTTGAAGGGGACA 12545
Qy 744 AGTACATTCAGAGAGAGGAATTCATGGGTAAAGTTCAGATTGTGGCTTGTGGGA 803
```

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Db 12546 GGCACTCCAG-----GCATAGGTAAAGATCTGTAGGTGTGCTTTGGGA 12593
Qy 804 TGAATTTCAAGTATTTCTGAAATGAAGACACCATGAAACAGGCGAGTGAAGATAT 863
Db 12594 TGAATTTCAAGTATTTCTGAAATGAAGACACCATGAAACAGGCGAGTGAAGATAT 12653
Qy 864 TTAAGAGCTTCAATGCCAATGGCTCCACTTCAAGTTTCTGATTAAGAACTCAGGTTCCGTGG 923
Db 12654 TTAATGATTTTATGCAATGGCTCCACTTCAAGTTTCTGATTAAGAACTCAGGTTCCGTGG 12713
Qy 924 ACTCCGATAAACATGATTAAGTTGTTATGATTCGCCATAGAAATTAAGTCAAGAGA 983
Db 12714 ACTCCGATTAACATTTGATTAAGTTGTTATGATTCGCCATAGAAATTAAGTCAAGAGA 12773
Qy 984 GGTAG--CAAGGGGTGTGTGCATCTT----- 1011
Db 12774 GGTCAATGATGGTGTGTGTGTATTTCTTGGCAATTCACAGGTGAGAAAGCTTTCC 12833
Qy 1012 -----TGCTACTGGCTGCAAGCTGACAGCTCCGCTCTCTTC 1045
Db 12834 AACTGACAGCAGACACAGGTGCCCTGCTACTGCTGACAGCTCCGCTCTCTTC 12893
Qy 1046 TCCAGCAGATTAACATTTGACAGCTTGAACCTAA--GACTGCTGACAGGCGAGGATGCT 1104
Db 12894 TCTAGCATTAATTAACATTCACAGCTCTCACTGATCACTGTGTGAGGCGAGAAAGCT 12953
Qy 1105 CAGGCGACAGGCCAGCAACACACACAGCAGTGAAGTAAAGTCAAGAGAGACAG 1164
Db 12954 CAGTGCACATAGCCAGCAAGAGCAACACAGAGCTGAAGAGAACTCAGAGAGAGAG 13013
Qy 1165 TTGAAGAGGCAAGTGGCATG 1186
Db 13014 ATAGTAGAGAAAGTAGTAGT 13035
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RESULT 8

```
US-10-121-960C-17
; Sequence 17, Application US/10121960C
; Publication No. US20030145341A1
; GENERAL INFORMATION:
; APPLICANT: ZHANG, Weisheng
; APPLICANT: PURCHIO, Anthony
; APPLICANT: HASHIMA, Sandy
; APPLICANT: MA, Shirley
; APPLICANT: NAMOTKA, Kevin
; TITLE OF INVENTION: ISOLATION AND IDENTIFICATION OF MOUSE AND HUMAN
; TITLE OF INVENTION: TRANSCRIPTION CONTROL ELEMENTS ASSOCIATED WITH
; FILE REFERENCE: 9400-0014 / PXE-014.US
; CURRENT APPLICATION NUMBER: US/10121,960C
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 15185
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CYP3A4-luc transgene
US-10-121-960C-17
```

```
Query Match 34.7%; Score 434.6; DB 15; Length 15185;
Best Local Similarity 76.1%; Pred. No. 4.9e-131;
Matches 646; Conservative 0; Mismatches 129; Indels 74; Gaps 6;

Qy 384 TCACCAAGACTCAGAGGATGACACAGAGGCGCCAGCAATCTCAACCAAGTCACTC 443
Db 12189 TCACCAAGAAAGTCAGAGGATGACATGACAGAGGCCAGCAATCTCAAGTCACTC 12248
Qy 444 CACCAACATTTCTGTCACCAACCATGTGTACAGTACCTGCTAGGGTCCAGGGTCACTGA 503
Db 12249 CACCAAGCTTTCTGTCACCAACCATGTGTGTACAGTACCTGCTAGGGGACAGGACATGA 12308
```


APPLICANT: Blomquist, Patrik
TITLE OF INVENTION: PROMOTER SEQUENCES
FILE REFERENCE: 13425-046001
CURRENT APPLICATION NUMBER: US/09/957,997
CURRENT FILING DATE: 2001-09-21
EARLIER APPLICATION NUMBER: SE 0003393-6
EARLIER FILING DATE: 2000-09-22
EARLIER APPLICATION NUMBER: 60/238,895
EARLIER FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 1012
TYPE: DNA
ORGANISM: Homo sapiens
US-09-957-997-4

Query Match 30.9%; Score 387.2; DB 9; Length 1012;
Best Local Similarity 79.3%; Pred. No. 4,3e-116;
Matches 530; Conservative 0; Mismatches 113; Indels 25; Gaps 5;

384 TCACCAAGACTGAGAGGGATGACACAGAGGGCCAGCAATCTCAACCAAGTCACTC 443
286 TCACCAAGAACTGAGAGGAATGACACAGAGGGCCAGCAATCTCAACCAAGTCACTC 345
444 CACCAACATTTCTGTGTCACCCACCATGTGTAACAGTACCTGCTGAGGGTCCAGGGTCAATGA 503
346 CACCAAGCTTTCTGTGTC-CCCACTGTGTGTAACAGTACCTGATAGGAGCCAGAGCCATGA 404
504 AAGTAATTAATACCAAGTGTGCTGCTGAGGAATCTCACTTGTGTAAGGAGAAACAGGAC 563
405 GAGTAATTAAGACCAAGCTATGCTGCTGAGAGTCACTTGTGTAAGGAGAAACAGGCTT 464
564 AGAAACCCCAAGAGGTGTGAGAGAGAAATGACAAATAGGACTGTGTAGAGGGGATAGG 623
465 GGAAGACACAAATGTGTGTAAGAGAAAGAAACAAATAGACTGTGATGAAGGGATGA 524
624 AGGCAACCAAGAGAGAAATGTGTACATCTGTGTGAGAGGTTGTGAAGAAAGACTTTA 683
525 AAGTCCCAAGAGAGAAATGTGTACATCTGTGTGAGAGGTTGTGAAGAAAGACTTTA 584
684 ATGAAAGGGGTCTGTGCTGCTGCTGCTGCAAGATGTGTGAGATCATTTAGGGGACCA 743
585 AGAGAA-GGCTGTGTGCTGCTGCTGCTGATGAAGATGTGTGAGATCTTTAGGGGACCA 643
744 AGTACATCTCAGAGAGAGGAATGTGATGAGTAAGATGTGCAATTTGCTTGTGAGG 803
644 GGCACTCTCAGAGAT------GGTAAAGATCTGTAGGATGCTTTTGGGA 691
804 TGAATTTCAAGTATTTGGAATGAAACAGCCATGAAACAAAGGAGGTGAGATAT 863
692 TGAATTTCAAGTATTTGGAATGAAACAGCCATGAGAC------AGAGAGAG 741
864 TTAAAGAGCTTCATGCAATGCTCCCACTTCAAGTTTGTGATTAAGATCAAGTCCGTGG 923
742 TTAAATATATTTTAAAGCAATGCTCCCACTTGAATTTGTGATTAAGATCAAGTCCGTGG 801
924 ACTCCCTGATTAAGATTAAGTTGTTATGATTTCCCAATAGATTAAGATCAAGAG 983
802 ACTCCCAAGTAACTTAATGATTTGATGATTTCTTAATTAAGATTAAGATCAAGAG 861
984 GGTAAAG-CAAGAGGGGTGTGCGATTTCTTGTCTAATGCTGAGCTGCAAGCCCGCTCC 1042
862 GGTCAAGTGAAGTGTGTGTGTGATTAATTTGCAATGCGAGGTGAGAAAGCTTTCC 921
1043 TTCTCCAG 1050
922 GACTGAG 929

RESULT 11
US-10-257-166-47
Sequence 47, Application US/10257166

Publication No. US20040023230A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPERROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Method and Nucleic Acids for Analysing the Methylation of
FILE REFERENCE: 5013.1011
CURRENT APPLICATION NUMBER: US/10/257,166
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: PCT/EP01/07470
DE 10032529.7
DE 10043826.1
PRIOR FILING DATE: 2001-06-29
2000-06-30
2000-09-01
NUMBER OF SEQ ID NOS: 178
SEQ ID NO 47
LENGTH: 8943
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-257-166-47

Query Match 20.2%; Score 253.4; DB 16; Length 8943;
Best Local Similarity 61.5%; Pred. No. 1.9e-71;
Matches 571; Conservative 0; Mismatches 276; Indels 82; Gaps 7;

384 TCACCAAGACTGAGAGGGATGACACAGAGGGCCAGCAATCTCAACCAAGTCACTC 443
4170 TTATTTAGAAAGTTAGAGAAATGATATATATATATATATATATATATATATATAT 4229
444 CACCAACATTTCTGTGTCACCCACCATGTGTAACCTGCTGAGGGTCCAGGGTCAATGA 503
4230 TATTTAGTTTTTTGCT-TTTTATGTGTATATATATATATATATATATATATATATATGA 4288
504 AAGTAATTAATACCAAGTGTGCTGCTGAGAACTCACTTGTCTAAGGAGAAACAGGAC 563
4289 GAGTGAATTAAGTATGATTTATTTTGTGAGAGTATTTTGTAAAGGAAATAGCTTT 4348
564 AGAAACCCCAAGAGGTGTGAGAGAGAAATGAGAAATAGCAATGATGTGAGGGGATAGG 623
4349 GGAATATTAATTAAGTGTGTAAGAGAAAGAAATTAATTAATTAATTAATTAATTAATGA 4408
624 AGCAACCAAGAGAGAAATGTGTAATCTGTGTGAGAGGTTGTGAAGAAAGACTTTA 683
4409 AAGTGTTAAGGAGAGAAATGTTATTTTGTGTGAGGGGTTGTGAGAAAGATTTTA 4468
684 ATGAAAGGGGTCTGTGCTGCTGCTGCTGCAAGATGTGTGAGATCTTAAGGGGACCA 743
4469 AGAGAA-GGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTA 4527
744 AGTACATCTCAGAGAGAGGAATGTGATGAGTAAGATGTGCAATTTGCTTGTGAGG 803
4528 GGTATATATTTAG------GTATAGTAAAGTTGTGATGATGTTGTGTTGGGA 4575
804 TGAATTTCAAGTATTTGGAATGAAACAGCCATGAAACAAAGGAGGTGAGAGATAT 863
4576 TGAATTTCAAGTATTTGGAATGAAACAGTATGTTAG------AGATTAAGAGAGAG 4625
864 TTAAAGAGCTTCATGCAATGCTCCCACTTCAAGTTTGTGATTAAGATCAAGTCCGTGG 923
4626 TTAAATATATTTTAAAGCAATGCTCCCACTTGAATTTGTGATTAAGATTTGAATTTTGG 4685
924 ACTCCCTGATTAAGATTAAGTTGTTATGATTTCCCAATAGATTAAGATCAAGAG 983
4686 ATTTTATTAATTAATTAAGTGTGTGATTTGATTAATTAATTAATTAATTAATTAATGA 4745
984 GGTAAAG-CAAGAGGGGTGTGCGATTTCTTGTCTAC------ 1017
4746 GGTATGAGTGTGTGTGTGTATTTTGTATATTTGTGAGGTGAGAAAGTTTTC 4805

Oy	1018	-----TTGGCTGACGTGCAGCCCGCCTCTCT	1046
Db	4806	GATTGTAGTAGAGACGGGGTTTTTGTATTTGGTTAGTTAAGTTTAAGTTTGTTTTTTTT	4865
Oy	1047	CCAGCACATAAACATTTTCAGCACTTGACTPA -GACTGCTGTGCAGGGCAGGAATGCTC	1105
Db	4866	TTAGTATTTAAATATTAATTAATAGTTTTTGTAAATTAATTTGTGTGTAAGGCTGGAAAAGTTT	4925
Oy	1106	CAGCGACAGCCCCGACCAACAACAGCACAGCTGAAAGTAMAGCTCAGAGGAGAAGT	1165
Db	4926	TATATATTTAATTAGTAATAGTAGTACGTTGTGAAAAAAGTTTTNAGAGAGAGAGA	4985
Oy	1166	TGAAGAAAGCAAGTGGCGATGACCTCATCCCAAATTTTGGCGGTGAAAACCTGGCTTCTC	1225
Db	4986	TMAAGAAAGAAAGAGATGATGATTTTATTTTAAATTTTGTCGTGGAATTTTGGTTTTTTT	5045
Oy	1226	CTGGCTGTCAAGCTGTGTCTCTCATAT	1254
Db	5046	TTGGTTGTAGTTGATATATTTTTTTATTTT	5074

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RESULT 12
US-10-257-166-48/c
; Sequence 48, Application US/10257166
; Publication No. US2004002330A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Method and Nucleic Acids for Analysing the Methylation of
; TITLE OF INVENTION: Genes Implicated in Pharmacogenomics
; FILE REFERENCE: 5013.1011
; CURRENT APPLICATION NUMBER: US/10/257,166
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: PCT/EP01/07470
; DE 10032529.7
; DE 10043826.1
; PRIOR FILING DATE: 2001-06-29
; 2000-06-30
; 2000-09-01
; NUMBER OF SEQ ID NOS: 178
; SEQ ID NO 48
; LENGTH: 8943
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; US-10-257-166-48

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Query Match	Similarity	Score	222.8	DB	Length	9943	
Best Local	Similarity	58.7%	Pred. No. 2.3e-61				
Match	546	Conservative	0	Mismatches	302	Indels	82
						Gaps	6
Qy	383	ATCACCAAGACTGAGGGGATGACACAGAGGGGCCGACAAATCTACCCAAAGTCACT					442
Db	4775	ATCACCAAAAAATCAAAAAAATAACACACAAAAACCAACAAATCTTACCAATCAACT					4716
Qy	443	CCACCAACATTTCTGTCATCCACCCACCATGTGTACATGACCTGCTAGGGTCAGGGTCATG					502
Db	4715	CCACCAACCTTTCTATC-CCCATATATATATACACACACCTTAATTAACCAAAACGATA					4657
Qy	503	AAAGTAATTAATACCACTGTGCCCTTGAGAACTCACTTGTGTAAGGAAACAGGCA					562
Db	4656	AAATTAATTAATAACCAACTATATACCTTAAAAAACTCACTCTACTAAAAAAACCAACC					4597
Qy	563	CAGAAACCCACAGGGGTGTAGAGGAAATAGACATTAGACTGTGTGAGGGGATNG					622
Db	4596	TAAAAACACACATATATATATAAAAAATAAAAAACAATAAAACATCAATAAAAAATTA					4537
Qy	623	GAGCAACCCAGAGGAGAAATGTTTACATCTGTGTGAGGAGGTTGTAGGAAGAAGCTTT					682
Db	4536	AAATATCCCAAAAAAATAATATATATCTTCTATATATAAAAAATATATATAAAAAACTCT					4477

QY	683	AATGAAGAGGGGTCTGTCTGGCTGGGCTTGCAGAGGATGTGAGAGTATCTAGGGGAC	742
Db	4476	AA-AAAAAAAACTATCTACTACTAATATATATAAAAAATATATAAAAATCTTCTAAAAAACAC	4418
QY	743	AAGTACACTCCAGGCAAGGGAATTGCATGGGTAAAGATGTGCAGTTGGCTTGTGGG	802
Db	4417	AAACACACTCCA-----AACTATAATTTAAATCTATTAACATACTTATTTAAA	4370
QY	803	ATGATTTTCAAGTATTCGTGGATGAAGACACGCCATGGAAAACAAGGCGAGAGGATA	862
Db	4369	ATTAATTTCAATATTTCTAAATATAAAAACAACCTAAAAACA-----AAAAAAA	4320
QY	863	TTTAAAGAGGCTTCAGCCCAATGGCTCCACCTTCAGTTTCTGATTAAGAACTCAGGTTCCGTG	922
Db	4319	ATTATTAATAATTTTATACCAATTAACCTCAACTTAATTTATATATATAAAAACCAAAACCTTA	4260
QY	923	GACTTCCTGATATAAACCTGATTAAGTTGTTATATGATTTCCCATAGATATATGACTCAAGG	982
Db	4259	AACCTCCCAATTAACATTAATTTAATAATTAATTTCTACATAAAAATTTAACTCAATAA	4200
QY	983	AGGTAAAGCAAGGGGTGTGTGCGATCTTGTG-----	1013
Db	4199	AAATCATTAATTAATATATATATATATTAATTTATTTACCACTACCGAAATAAAAAACTCTTC	4140
QY	1014	-----CTACTGGCTGCAGCTGCAGCCCCGCTCTTC	1045
Db	4139	CGACTACAAAACAAAACAGAAAACCTACTACTAATCAATCAACCTCAACCTCACTCTTC	4080
QY	1046	TCGACGACATTAACATTTTCAGCACTGACCTTA-GACTGCTGTGCGAGGCGAGGATGCT	1104
Db	4079	TTCAACACTATTAACAAATTCCAACCACTCACTAAATTCCTACTATATACAAAACAAAAAACT	4020
QY	1105	CCAGGACGACAGCCCGACCAAAACAACACACACACAGCTAAAGTAAGACTCAGAGAGACAG	1164
Db	4019	CCAACACACAAACCCCAACAAACAAACAAACACACGCTACTAAAAAAAACCTCAAAAAAAA	3960
QY	1165	TTGAAGAAAGCAAGTGGCGATGGACTTCATCCAAATTTGGCGGTGAAAACCTGGCTTCT	1224
Db	3959	ATTAATAAAAAAATAATTAATTAATTAATTCATCTCCAAACTTAACCTTAATAAAACCTAACCTTCT	3900
QY	1225	CGTGGCTGTACGCTGGGCTCCCTCTAATCT	1254
Db	3899	CCTAATCTATCAACTTAATTAATCTCTCTAATCT	3870

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RESULT 13
US-09-880-107-2114
; Sequence 2114, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, DarcI T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Schert, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2114
; LENGTH: 1707
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 J04813
US-09-880-107-2114

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Best Local Similarity 93.7%; Pred. No. 3.8e-35;
Matches 148; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Qy 1097 GGATGCTCCAGGAGAGAGCCGCAAAACAGACAGCTGAAGAAGTCACTGAGA 1156
Db 1 GGGAGCTCCAGGAGAGAGCCGCAAAACAGACAGCTGAAGAAGTCACTGAGA 60
Qy 1157 GGAGACAGTTGAAGAAGGCAAGTGGCGATGAGACCTCATCCAAATTTGGCGGTGAAAAC 1216
Db 61 GAACACAGTTGAAGAAGGCAAGTGGCGATGAGACCTCATCCAAATTTGGCGGTGAAAAC 120
Qy 1217 TGGCTTCCTCGGCTGTGACGCTGTGCTCTATCT 1254
Db 121 TGGCTTCCTCGGCTGTGACGCTGTGCTCTATCT 158

RESULT 14
US-10-641-643-1060
Sequence 1060, Application US/10641643
Publication No. US20040077003A1
GENERAL INFORMATION:
APPLICANT: Cocke, Benjamin G.
Jeffrey J. Seilhamer
Susan G. Stuart
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
GENE EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/641,643
FILING DATE: 14-Aug-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1060:
SEQUENCE CHARACTERISTICS:
LENGTH: 1707 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g181345
SEQUENCE DESCRIPTION: SEQ ID NO: 1060 :
US-10-641-643-1060

Query Match 11.3%; Score 142; DB 16; Length 1707;
Best Local Similarity 93.7%; Pred. No. 3.8e-35;
Matches 148; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Qy 1097 GGATGCTCCAGGAGAGAGCCGCAAAACAGACAGCTGAAGAAGTCACTGAGA 1156
Db 1 GGGAGCTCCAGGAGAGAGCCGCAAAACAGACAGCTGAAGAAGTCACTGAGA 60

Qy 1157 GGAGACAGTTGAAGAAGGCAAGTGGCGATGAGACCTCATCCAAATTTGGCGGTGAAAAC 1216
Db 61 GAACACAGTTGAAGAAGGCAAGTGGCGATGAGACCTCATCCAAATTTGGCGGTGAAAAC 120
Qy 1217 TGGCTTCCTCGGCTGTGACGCTGTGCTCTATCT 1254
Db 121 TGGCTTCCTCGGCTGTGACGCTGTGCTCTATCT 158

RESULT 15
US-09-925-297-24
Sequence 24, Application US/09925297
Patent No. US20020081659A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA105
CURRENT APPLICATION NUMBER: US/09/925,297
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 24
LENGTH: 384
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (357)
OTHER INFORMATION: n equals a,t,g, or c
US-09-925-297-24

Query Match 11.2%; Score 141; DB 9; Length 384;
Best Local Similarity 93.6%; Pred. No. 3.4e-35;
Matches 147; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Qy 1098 GGATGCTCCAGGAGAGAGCCGCAAAACAGACAGCTGAAGAAGTCACTGAGA 1157
Db 1 GGAAGCTCCAGGAGAGAGCCGCAAAACAGACAGCTGAAGAAGTCACTGAGA 60
Qy 1158 GGAGACAGTTGAAGAAGGCAAGTGGCGATGAGACCTCATCCAAATTTGGCGGTGAAAAC 1217
Db 61 AACACAGTTGAAGAAGGCAAGTGGCGATGAGACCTCATCCAAATTTGGCGGTGAAAAC 120
Qy 1218 GGGCTTCCTCGGCTGTGACGCTGTGCTCTATCT 1254
Db 121 GGGCTTCCTCGGCTGTGACGCTGTGCTCTATCT 157

Search completed: January 26, 2005, 19:49:30
Job time : 635.441 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 26, 2005, 13:23:32 ; Search time 4.22069 Seconds
(without alignments)
8588.699 Million cell updates/sec

Title: SEQ4-1010-1060-1037G

Perfect score: 51
Sequence: 1 ttctgcacacgctgcacgctg.....ccttcgcacacataaaca 51

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 1: /cgn2_6/ptodaca/1/ina/5A.COMB.seq:*
- 2: /cgn2_6/ptodaca/1/ina/5B.COMB.seq:*
- 3: /cgn2_6/ptodaca/1/ina/6A.COMB.seq:*
- 4: /cgn2_6/ptodaca/1/ina/6B.COMB.seq:*
- 5: /cgn2_6/ptodaca/1/ina/PTCUS.COMB.seq:*
- 6: /cgn2_6/ptodaca/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39.4	77.3	1345	US-09-372-339-1	Sequence 1, Appli
2	39.4	77.3	1345	US-09-372-339-2	Sequence 2, Appli
3	39.4	77.3	1345	US-09-144-367-3	Sequence 3, Appli
4	27	52.9	873	US-09-252-991A-5146	Sequence 5146, Ap
5	27	52.9	981	US-09-252-991A-5003	Sequence 5003, Ap
6	27	52.9	1581	US-09-252-991A-5177	Sequence 5177, Ap
7	26.2	51.4	320	US-09-513-999C-33490	Sequence 33490, A
8	26.2	51.4	1578	US-09-252-991A-5039	Sequence 5039, Ap
9	25.4	49.8	2292	US-09-270-767-15045	Sequence 15045, A
10	25.2	49.4	927	US-09-248-796A-246	Sequence 246, App
11	25	49.0	6674	US-09-620-312D-110	Sequence 110, App
12	24.8	48.6	1588	US-09-490-291-7	Sequence 7, Appli
13	24.8	48.6	2338	US-08-425-069-1	Sequence 1, Appli
14	24.8	48.6	2338	US-08-317-844B-1	Sequence 13706, A
15	24.8	48.6	3246	US-09-270-767-13706	Sequence 13706, A
16	24.4	47.8	445	US-09-270-767-6152	Sequence 6152, Ap
17	24.4	47.8	445	US-09-270-767-21434	Sequence 21434, A
18	24.4	47.8	3028	US-09-392-714-2	Sequence 2, Appli
19	24.2	47.5	795	US-09-795-926-47	Sequence 47, Appli
20	24.2	47.5	4182	US-07-973-257-1	Sequence 1, Appli
21	24	47.1	2190	US-09-270-767-26507	Sequence 26507, A
22	24	47.1	2366	US-09-799-451-351	Sequence 351, App
23	24	47.1	2760	US-09-270-767-13149	Sequence 13149, A
24	24	47.1	2913	US-09-270-767-11002	Sequence 11002, A
25	23.8	46.7	511	US-09-556-877-271	Sequence 271, App
26	23.8	46.7	511	US-09-620-412C-271	Sequence 271, App
27	23.8	46.7	511	US-09-598-419-271	Sequence 271, App

C	28	23.8	46.7	831	4	US-09-252-991A-5118	Sequence 5118, Ap
	29	23.8	46.7	1965	4	US-09-620-412C-340	Sequence 340, App
	30	23.8	46.7	1965	4	US-09-598-419-340	Sequence 340, App
C	31	23.8	46.7	2900	4	US-09-620-312D-673	Sequence 673, App
	32	23.8	46.7	5265	4	US-09-556-877-174	Sequence 174, App
	33	23.8	46.7	5265	4	US-09-556-877-174	Sequence 174, App
	34	23.8	46.7	5265	4	US-09-556-877-174	Sequence 174, App
	35	23.8	46.7	229354	4	US-09-598-419-174	Sequence 174, App
	36	23.8	46.7	229354	4	US-09-598-419-174	Sequence 174, App
	37	23.8	46.7	4403765	3	US-09-765-400-64	Sequence 64, Appl
	38	23.8	46.7	4403765	3	US-09-765-400-64	Sequence 64, Appl
	39	23.4	45.9	535	3	US-09-103-840A-2	Sequence 2, Appli
C	40	23.4	45.9	535	3	US-09-056-556-171	Sequence 171, Appl
	41	23.4	45.9	535	4	US-09-072-596-166	Sequence 166, App
C	42	23.4	45.9	1989	1	US-09-072-596-166	Sequence 171, App
	43	23.4	45.9	1989	1	US-08-447-500-5	Sequence 5, Appli
	44	23.4	45.9	1989	1	US-08-454-097-5	Sequence 5, Appli
	45	23.4	45.9	1989	3	US-08-453-866-5	Sequence 5, Appli

ALIGNMENTS

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RESULT 1
US-09-372-339-1
Sequence 1, Application US/09372339
Patent No. 6174684
GENERAL INFORMATION:
APPLICANT: Redbeck, Timothy
APPLICANT: Redbeck, Timothy
TITLE OF INVENTION: CYP3A4 NFSE Variant and Methods of Use Therefor
FILE REFERENCE: PENN-0695
CURRENT APPLICATION NUMBER: US/09/372.339
CURRENT FILING DATE: 1999-08-11
EARLIER APPLICATION NUMBER: 60/096,586
EARLIER FILING DATE: 1998-08-14
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 1345
TYPE: DNA
ORGANISM: Homo sapiens
US-09-372-339-1

Query Match      77.3%; Score 39.4; DB 3; Length 1345;
Best Local Similarity 87.8%; Pred. No. 0.00039;
Matches 43; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Cy      3 TGCTACTGCTGAGCTGACGCCACCTCTCTGACGACATTAACA 51
Db      1035 TGCTACTGCTGAGCTGACGCCACCTCTCTCTGACGACATTAACA 1083

RESULT 2
US-09-372-339-2
Sequence 2, Application US/09372339
Patent No. 6174684
GENERAL INFORMATION:
APPLICANT: Redbeck, Timothy
APPLICANT: Redbeck, Timothy
TITLE OF INVENTION: CYP3A4 NFSE Variant and Methods of Use Therefor
FILE REFERENCE: PENN-0695
CURRENT APPLICATION NUMBER: US/09/372.339
CURRENT FILING DATE: 1999-08-11
EARLIER APPLICATION NUMBER: 60/096,586
EARLIER FILING DATE: 1998-08-14
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 1345
TYPE: DNA
ORGANISM: Homo sapiens
US-09-372-339-2
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Query Match 77.3%; Score 39.4; DB 3; Length 1345;
Best Local Similarity 87.8%; Pred. No. 0.00039;
Matches 43; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 TGCTACTGGCTGCAGCTGCAGCCCCCACCCTCTTCTGCAGCACAATAACA 51
Db 1035 TGCTACTGGCTGCAGCTGCAGCCCCCACCCTCTTCTGCAGCACAATAACA 1083

RESULT 3

US-09-144-367-3
; Sequence 3, Application US/09144367
; Patent No. 6432639
; GENERAL INFORMATION:
; APPLICANT: Lichter, Jay
; APPLICANT: Guido, Marco
; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
; FILE REFERENCE: SEQ-12P
; CURRENT APPLICATION NUMBER: US/09/144,367
; CURRENT FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/058,612
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: Other
; LOCATION: (0)...(0)
US-09-144-367-3

Query Match 77.3%; Score 39.4; DB 4; Length 1345;
Best Local Similarity 87.8%; Pred. No. 0.00039;
Matches 43; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 TGCTACTGGCTGCAGCTGCAGCCCCCACCCTCTTCTGCAGCACAATAACA 51
Db 1035 TGCTACTGGCTGCAGCTGCAGCCCCCACCCTCTTCTGCAGCACAATAACA 1083

RESULT 4

US-09-252-991A-5146/C
; Sequence 5146, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5146
; LENGTH: 873
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5146

Query Match 52.9%; Score 27; DB 4; Length 873;
Best Local Similarity 70.6%; Pred. No. 4.4;
Matches 36; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 TTTGCTACTGGCTGCAGCTGCAGCCCCCACCCTCTTCTGCAGCACAATAACA 51
Db 70 TTGCTCATGCTGCAGCTGCAGCTGCAGCCCCCACCCTCTTCTGCAGCACAATAACA 20

RESULT 5
US-09-252-991A-5003
; Sequence 5003, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5003
; LENGTH: 981
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5003

Query Match 52.9%; Score 27; DB 4; Length 981;
Best Local Similarity 70.6%; Pred. No. 4.5;
Matches 36; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 TTTGCTACTGGCTGCAGCTGCAGCCCCCACCCTCTTCTGCAGCACAATAACA 51
Db 140 TTGCTCATGCTGCAGCTGCAGCTGCAGCCCCCACCCTCTTCTGCAGCACAATAACA 190

RESULT 6

US-09-252-991A-5177/C
; Sequence 5177, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5177
; LENGTH: 1581
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5177

Query Match 52.9%; Score 27; DB 4; Length 1581;
Best Local Similarity 70.6%; Pred. No. 5.1;
Matches 36; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 TTTGCTACTGGCTGCAGCTGCAGCCCCCACCCTCTTCTGCAGCACAATAACA 51
Db 141 TTGCTCATGCTGCAGCTGCAGCTGCAGCCCCCACCCTCTTCTGCAGCACAATAACA 91

RESULT 7

US-09-513-999C-33490/C
; Sequence 33490, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961


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FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513.999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 33490
LENGTH: 320
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 2
OTHER INFORMATION: r=a or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: 12
OTHER INFORMATION: r=a or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: 14
OTHER INFORMATION: r=a or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: 205
OTHER INFORMATION: r=a or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: 171
OTHER INFORMATION: s=g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: 282
OTHER INFORMATION: w=a or t
US-09-513.999C-33490

Query Match 51.4%; Score 26.2; DB 4; Length 320;
Best Local Similarity 69.4%; Pred. No. 6.4;
Matches 34; Conservative 1; Mismatches 14; Indels 0; Gaps 0;

QY 2 TTGCTACTGGCTGCTGAGCGCCCACTCTTCTGACAGACATAAC 50
Db 173 TCCCGCTGACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 125

RESULT 8
US-09-252-991A-5039
Sequence 5039, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252.991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 5039
LENGTH: 1578
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5039

Query Match 51.4%; Score 26.2; DB 4; Length 1578;
Best Local Similarity 72.3%; Pred. No. 9.3;
Matches 34; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 TTGCTACTGGCTGCTGAGCGCCCACTCTTCTGACAGACATA 47
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Db 1531 TTGCTACTGGCTGCTGAGCGCCCACTCTTCTGACAGACATA 1577

RESULT 9
US-09-270-767-15045/C
Sequence 15045, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270.767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentn Ver. 2.0
SEQ ID NO 15045
LENGTH: 2292
TYPE: DNA
ORGANISM: Drosophila melanogaster
US-09-270-767-15045

Query Match 49.8%; Score 25.4; DB 4; Length 2292;
Best Local Similarity 68.6%; Pred. No. 19;
Matches 35; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 TTGCTACTGGCTGCTGAGCGCCCACTCTTCTGACAGACATA 51
Db 240 TTGATTTGGCTGCTGAGCTTCAGCTCCAGCTCCAGCTGAGCTGCGCA 190

RESULT 10
US-09-248-796A-246
Sequence 246, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248.796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 246
LENGTH: 927
TYPE: DNA
ORGANISM: Candida albicans
US-09-248-796A-246

Query Match 49.4%; Score 25.2; DB 4; Length 927;
Best Local Similarity 71.7%; Pred. No. 18;
Matches 33; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 3 TGGCTACTGGCTGCTGAGCGCCCACTCTTCTGACAGACATA 48
Db 749 TGGCAGCGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 794

RESULT 11
US-09-620-312D-110
Sequence 110, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Amandl, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
```

```

; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yungqing
; APPLICANT: Wang, Duntui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662e1 Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pc_Fl_genes Version 1.0
; SEQ ID NO 110
; LENGTH: 6674
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1312)..(6330)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(6674)
; OTHER INFORMATION: n = a,t,c or g
; US-09-620-312D-110

Query Match          49.0%; Score 25; DB 4; Length 6674;
Best Local Similarity 75.6%; Pred. No. 33;
Matches 31; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy      4 GCTACTGAGCTGCAGCTGCAGCCGACCTCTTGTGACAGC 44
Db      1328 GCGTCTGGCTGCTGCTGCTGCGCCGCCCTTGTCTCCAC 1368

RESULT 12
US-09-490-291-7/c
; Sequence 7, Application US/09490291
; Patent No. 6620917
; GENERAL INFORMATION:
; APPLICANT: Mello, Charlene M.
; APPLICANT: Arcidiacono, Steven
; TITLE OF INVENTION: No. 6620917e1 Purification and Fiber Spinning Techniques for
; TITLE OF INVENTION: Protein Fibers
; FILE REFERENCE: ARMY-03665
; CURRENT APPLICATION NUMBER: US/09/490,291
; CURRENT FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1588
; TYPE: DNA
; ORGANISM: Nephila clavipes
; US-09-490-291-7

Query Match          48.6%; Score 24.8; DB 4; Length 1588;
Best Local Similarity 80.6%; Pred. No. 27;
Matches 29; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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Qy      11 GCTGACGCTGCAGCCGACCTCTTGTGACAGC 46
Db      1121 GCTGACGCGGCTGCTCCAGCTCTTGTCCAGACACT 1086
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RESULT 13
US-08-425-069-1/c
; Sequence 1, Application US/08425069
; Patent No. 5728810
; GENERAL INFORMATION:
; APPLICANT: Lewis, Randolph V.
; APPLICANT: Xu, Ming
; APPLICANT: Himmam, Michael B.
; TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
; TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
; TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolaach & Birch
; STREET: 301 No. 5728810th Washington Street
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22046
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,069
; FILING DATE: 19-Apr-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1447-106P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2338 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Nephila clavipes
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2154
; OTHER INFORMATION: /product= "Nephila clavipes
; OTHER INFORMATION: dragline silk protein"
; PUBLICATION INFORMATION:
; AUTHORS: Xu, Ming
; AUTHORS: Lewis, Randolph V.
; TITLE: Structure of a protein superfiber: Spider
; TITLE: dragline silk
; JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
; VOLUME: 87
; PAGES: 7120-7124
; DATE: Sept.-1990
; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 2338
; US-08-425-069-1

Query Match          48.6%; Score 24.8; DB 1; Length 2338;
Best Local Similarity 80.6%; Pred. No. 30;
Matches 29; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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Qy      11 GCTGACGCTGCAGCCGACCTCTTGTGACAGC 46
Db      1697 GCTGACGCGGCTGCTCCAGCTCTTGTCCAGACACT 1662
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RESULT 14

US-08-317-844B-1/c
Sequence 1, Application US/08317844B
Patent No. 5989894
GENERAL INFORMATION:
APPLICANT: Lewis, Randolph V.
APPLICANT: Xu, Ming
APPLICANT: Himmann, Michael B.
TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 301 No. 5989894th Washington Street
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22046
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,844B
FILING DATE: 04-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1447-105P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 241-1300
TELEFAX: (703) 241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 238 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Nephilia clavipes
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2154
OTHER INFORMATION: /product= "Nephilia clavipes"
OTHER INFORMATION: drasline silk protein"
PUBLICATION INFORMATION:
AUTHORS: Xu, Ming
AUTHORS: Lewis, Randolph V.
TITLE: Structure of a protein superfiber: Spider
TITLE: drasline silk
JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
VOLUME: 87
PAGES: 7120-7124
DATE: Sept.-1990
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 2338
US-08-317-844B-1

Query Match 48.6%; Score 24.8; DB 2; Length 2338;
Best Local Similarity 80.6%; Pred. No. 30;
Matches 29; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 11 GCTGAGCTGAGCCGACCTCTCTGACGACAT 46
DB 1697 GCTGAGCGGCTGCTCCAGCTCTGTCCAGACCT 1662

RESULT 15
US-09-270-767-13706

Sequence 13706, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13706
LENGTH: 3246
TYPE: DNA
ORGANISM: Drosophila melanogaster
US-09-270-767-13706

Query Match 48.6%; Score 24.8; DB 4; Length 3246;
Best Local Similarity 72.7%; Pred. No. 32;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 3 TGCTACTGCTGAGCTGAGCCGACCTCTCTGACGACAT 46
DB 306 TGATTAATGTCGAGCTGAGCGGCACTTCTTCATCTCCT 349

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OM nucleic - nucleic search, using sw model

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- 5: /cgn2_6/prodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/prodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/prodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq:*
- 10: /cgn2_6/prodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/prodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/prodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/prodata/1/pubpna/US10E_PUBCOMB.seq:*
- 17: /cgn2_6/prodata/1/pubpna/US10F_PUBCOMB.seq:*
- 18: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq:*
- 19: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49.4	96.9	1254	14	US-10-085-612-4
2	41	80.4	1012	9	US-09-957-997-4
3	41	80.4	1186	9	US-09-957-997-1
4	39.4	77.3	1345	10	US-09-943-115A-1
5	39.4	77.3	1345	14	US-10-146-575-3
6	39.4	77.3	1345	14	US-10-085-612-3
7	39.4	77.3	13035	15	US-10-121-960C-14
8	39.4	77.3	15185	15	US-10-121-960C-17
9	31.4	61.6	8943	16	US-10-257-166-48
10	29.8	58.4	8766	16	US-10-257-166-150
11	28	54.9	34	14	US-10-085-612-6
12	27.2	53.3	4130	17	US-10-775-169-80

C	13	27.2	53.3	8575	10	US-09-764-891-8707	Sequence 8707, Ap
C	14	27	52.9	34	14	US-10-085-612-2	Sequence 2, Appl
C	15	26.6	52.2	704	18	US-10-425-115-176951	Sequence 176951,
C	16	25.8	50.6	12614	15	US-10-242-355-1086	Sequence 1086, Ap
C	17	25.8	50.2	22314	17	US-10-322-281-164	Sequence 164, App
C	18	25.6	50.2	306	17	US-10-437-963-70996	Sequence 70996, A
C	19	25.6	50.2	384	16	US-10-424-599-115210	Sequence 115210,
C	20	25.6	50.2	493	11	US-09-732-627A-2583	Sequence 2583, Ap
C	21	25.6	50.2	572	13	US-10-027-633-196479	Sequence 196479,
C	22	25.6	50.2	572	15	US-10-027-632-196479	Sequence 196479,
C	23	25.6	50.2	1158	15	US-10-369-493-36839	Sequence 36839, A
C	24	25.6	50.2	3015	16	US-10-263-923-43	Sequence 43, Appl
C	25	25.4	49.8	259	10	US-09-764-891-7918	Sequence 7918, Ap
C	26	25.4	49.8	627	9	US-09-770-149-726	Sequence 726, App
C	27	25.4	49.8	5541	10	US-09-930-219-272	Sequence 272, App
C	28	25.4	49.8	5541	15	US-10-341-434-74	Sequence 74, Appl
C	29	25.4	49.8	5541	18	US-10-622-377-9	Sequence 9, Appl
C	30	25.4	49.8	5612	16	US-10-276-774-846	Sequence 846, App
C	31	25.4	49.8	31364	17	US-10-741-601-5672	Sequence 5672, Ap
C	32	25.4	49.8	53331	17	US-10-741-601-5762	Sequence 5762, Ap
C	33	25.2	49.0	160	16	US-10-424-599-83796	Sequence 83796, A
C	34	25	49.0	402	10	US-09-764-891-2198	Sequence 2198, Ap
C	35	25	49.0	871	13	US-10-027-632-168228	Sequence 168228,
C	36	25	49.0	871	15	US-10-027-632-168228	Sequence 168228,
C	37	25	49.0	5010	10	US-09-918-715-251	Sequence 251, App
C	38	25	49.0	5010	15	US-10-172-118-680	Sequence 680, App
C	39	25	49.0	5010	16	US-10-342-887-680	Sequence 680, App
C	40	25	49.0	5010	18	US-10-474-794-251	Sequence 251, App
C	41	25	49.0	5662	15	US-10-084-817-91	Sequence 91, Appl
C	42	25	49.0	6021	10	US-09-814-352-20075	Sequence 20075, A
C	43	25	49.0	6021	14	US-10-198-846-10879	Sequence 10879, A
C	44	25	49.0	6447	16	US-10-159-563-133	Sequence 133, App
C	45	25	49.0	6674	15	US-10-037-270-110	Sequence 110, App

ALIGNMENTS

RESULT 1
US-10-085-612-4
Sequence 4, Application US/10085612
Publication No. US20030096251A1
GENERAL INFORMATION:
APPLICANT: Guida, Marco
APPLICANT: Hall, Jeff
APPLICANT: Petros, William
APPLICANT: Vredenburg, James
APPLICANT: Colvin, Oliver
APPLICANT: Marks, Jeffrey
TITLE OF INVENTION: Methods for Evaluating the Ability to Metabolize Pharmaceuticals
FILE REFERENCE: 4389-5-Cl
CURRENT APPLICATION NUMBER: US/10/085,612
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 09/144,367
PRIOR FILING DATE: 1998-08-31
PRIOR APPLICATION NUMBER: 60/271,630
PRIOR FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 1254
TYPE: DNA
ORGANISM: Homo sapiens
US-10-085-612-4

Query Match: 96.9%; Score 49.4; DB 14; Length 1254;
Best Local Similarity: 98.0%; Pred. No. 3; 1e-07;
Matches 50; Conservative 0; Mismatches 1; Indels 0;
Gaps 0;
Db 1010 TTGCTACTGGCTGCAGCTGCAGCCCACTCTTCTGCAGCATATAACA 51
1010 TTGCTACTGGCTGCAGCTGCAGCCCACTCTTCTGCAGCATATAACA 1060

RESULT 2
US-09-957-997-4
; Sequence 4, Application US/09957997
; Patent No. US20020150915A1
; GENERAL INFORMATION:
; APPLICANT: Berkenstam, Anders
; APPLICANT: Blomquist, Patrik
; APPLICANT: Blomquist, Patrik
; TITLE OF INVENTION: PROMOTER SEQUENCES
; FILE REFERENCE: 13425-046001
; CURRENT APPLICATION NUMBER: US/09/957,997
; CURRENT FILING DATE: 2001-09-21
; EARLIER APPLICATION NUMBER: SE 0003393-6
; EARLIER FILING DATE: 2000-09-22
; EARLIER APPLICATION NUMBER: 60/238,895
; EARLIER FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1012
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-957-997-4

Query Match 80.4%; Score 41; DB 9; Length 1012;
Best Local Similarity 89.8%; Pred. No. 0.00022;
Matches 44; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 TGCTACTGGCTGCGAGCTGCAGCCCACTCTTCTTGACGACATTAACA 51
Db 947 TGCTACTGGCTGCGAGCTGCAGCCCTGCTCTCTCCAGCATTAACA 995

RESULT 3
US-09-957-997-1
; Sequence 1, Application US/09957997
; Patent No. US20020150915A1
; GENERAL INFORMATION:
; APPLICANT: Berkenstam, Anders
; APPLICANT: Blomquist, Patrik
; APPLICANT: Blomquist, Patrik
; TITLE OF INVENTION: PROMOTER SEQUENCES
; FILE REFERENCE: 13425-046001
; CURRENT APPLICATION NUMBER: US/09/957,997
; CURRENT FILING DATE: 2001-09-21
; EARLIER APPLICATION NUMBER: SE 0003393-6
; EARLIER FILING DATE: 2000-09-22
; EARLIER APPLICATION NUMBER: 60/238,895
; EARLIER FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1186
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-957-997-1

Query Match 80.4%; Score 41; DB 9; Length 1186;
Best Local Similarity 89.8%; Pred. No. 0.00027;
Matches 44; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 TGCTACTGGCTGCGAGCTGCAGCCCACTCTTCTTGACGACATTAACA 51
Db 11064 TGCTACTGGCTGCGAGCTGCAGCCCTGCTCTCTCCAGCATTAACA 11112

RESULT 4
US-09-943-115A-1
; Sequence 1, Application US/09943115A
; Publication No. US20030017469A1
; GENERAL INFORMATION:

APPLICANT: SEQUENOM, Inc.
; APPLICANT: Risinger, Carl
; APPLICANT: Andersson, Maria
; APPLICANT: Lewander, Tommy
; APPLICANT: Olsson, Erik
; TITLE OF INVENTION: DETECTION OF CYP3A4 AND CYP2C9
; FILE REFERENCE: 52459-20021.00
; CURRENT APPLICATION NUMBER: US/09/943,115A
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: UK 0021286.0
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-943-115A-1

Query Match 77.3%; Score 39.4; DB 10; Length 1345;
Best Local Similarity 87.8%; Pred. No. 0.00079;
Matches 43; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 TGCTACTGGCTGCGAGCTGCAGCCCACTCTTCTTGACGACATTAACA 51
Db 1035 TGCTACTGGCTGCGAGCTGCAGCCCTGCTCTCTCTAGCATTAACA 1083

RESULT 5
US-10-146-575-3
; Sequence 3, Application US/10146575
; Publication No. US20030059800A1
; GENERAL INFORMATION:
; APPLICANT: Lichter, Jay
; APPLICANT: Guido, Marco
; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
; FILE REFERENCE: SEQ-12P
; CURRENT APPLICATION NUMBER: US/10/146,575
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US/09/144,367
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: Other
; LOCATION: (0)...(0)
US-10-146-575-3

Query Match 77.3%; Score 39.4; DB 14; Length 1345;
Best Local Similarity 87.8%; Pred. No. 0.00079;
Matches 43; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 TGCTACTGGCTGCGAGCTGCAGCCCACTCTTCTTGACGACATTAACA 51
Db 1035 TGCTACTGGCTGCGAGCTGCAGCCCTGCTCTCTCTAGCATTAACA 1083

RESULT 6
US-10-085-612-3
; Sequence 3, Application US/10085612
; Publication No. US20030096251A1
; GENERAL INFORMATION:
; APPLICANT: Guida, Marco
; APPLICANT: Hall, Jeff
; APPLICANT: Petros, William
; APPLICANT: Vredenburg, James
; APPLICANT: Colvin, Oliver
; APPLICANT: Marks, Jeffrey

```

; TITLE OF INVENTION: Methods for Evaluating the Ability to Metabolize Pharmaceuticals
; FILE OF INVENTION: Compositions Therefor
; FILE REFERENCE: 4389-5-C1
; CURRENT APPLICATION NUMBER: US/10/085,612
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/144,367
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/271,630
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION: Description of Artificial Sequence: human CYP3A4 gene locus
US-10-085-612-3

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Query Match 77.3%; Score 39.4; DB 14; Length 1345;
Best Local Similarity 87.8%; Pred. No. 0.00079;
Matches 43; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Cy 3 TGCCTAGGCTGCGAGCTGCGAGCCCGACCTCTCTTCTGCGAGCATTAACA 51
Db 1035 TGCCTAGGCTGCGAGCTGCGAGCCCGACCTCTCTCTCTGCGATTAACA 1083

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RESULT 7

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US-10-121-960C-14
; Sequence 14, Application US/10121960C
; Publication No. US20030145341A1
; GENERAL INFORMATION:
; APPLICANT: ZHANG, Weisheng
; APPLICANT: ZHANG, Pamela
; APPLICANT: PURCHIO, Anthony
; APPLICANT: HASHIMA, Sandy
; APPLICANT: MA, Shitley
; APPLICANT: NAMOTKA, Kevin
; TITLE OF INVENTION: ISOLATION AND IDENTIFICATION OF MOUSE AND HUMAN
; TITLE OF INVENTION: TRANSCRIPTION CONTROL ELEMENTS ASSOCIATED WITH
; TITLE OF INVENTION: CYTOCHROME EXPRESSION
; FILE REFERENCE: 9400-0014 / PXE-014.US
; CURRENT APPLICATION NUMBER: US/10/121,960C
; CURRENT FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 13035
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human CYP3A4 gene locus
US-10-121-960C-14

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Query Match 77.3%; Score 39.4; DB 15; Length 13035;
Best Local Similarity 87.8%; Pred. No. 0.00097;
Matches 43; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Cy 3 TGCCTAGGCTGCGAGCTGCGAGCCCGACCTCTCTTCTGCGAGCATTAACA 51
Db 12860 TGCCTAGGCTGCGAGCTGCGAGCCCGACCTCTCTCTCTGCGATTAACA 12908

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RESULT 8

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US-10-121-960C-17
; Sequence 17, Application US/10121960C
; Publication No. US20030145341A1
; GENERAL INFORMATION:
; APPLICANT: ZHANG, Weisheng
; APPLICANT: PURCHIO, Anthony
; APPLICANT: HASHIMA, Sandy
; APPLICANT: MA, Shitley
; APPLICANT: NAMOTKA, Kevin

```

```

; TITLE OF INVENTION: ISOLATION AND IDENTIFICATION OF MOUSE AND HUMAN
; FILE OF INVENTION: TRANSCRIPTION CONTROL ELEMENTS ASSOCIATED WITH
; FILE REFERENCE: 9400-0014 / PXE-014.US
; CURRENT APPLICATION NUMBER: US/10/121,960C
; CURRENT FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 15185
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CYP3A4-luc transgene
US-10-121-960C-17

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Query Match 77.3%; Score 39.4; DB 15; Length 15185;
Best Local Similarity 87.8%; Pred. No. 0.00098;
Matches 43; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Cy 3 TGCCTAGGCTGCGAGCTGCGAGCCCGACCTCTCTTCTGCGAGCATTAACA 51
Db 12860 TGCCTAGGCTGCGAGCTGCGAGCCCGACCTCTCTCTCTGCGATTAACA 12908

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RESULT 9

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US-10-257-166-48/C
; Sequence 48, Application US/10257166
; Publication No. US20040023230A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Method and Nucleic Acids for Analysing the Methylation of
; TITLE OF INVENTION: Genes Implicated in Pharmacogenomics
; FILE REFERENCE: 5013.1011
; CURRENT APPLICATION NUMBER: US/10/257,166
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: PCT/EP01/07470
; DE 10032529.7
; DE 10043826.1
; PRIOR FILING DATE: 2001-06-29
; 2000-06-30
; 2000-09-01
; NUMBER OF SEQ ID NOS: 178
; SEQ ID NO 48
; LENGTH: 8943
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-257-166-48

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Query Match 61.6%; Score 31.4; DB 16; Length 8943;
Best Local Similarity 77.6%; Pred. No. 0.49;
Matches 38; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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Cy 3 TGCCTAGGCTGCGAGCTGCGAGCCCGACCTCTTCTGCGAGCATTAACA 51
Db 4113 TACTACTAATCACTACCACTCACTCTCTCTCCACATTAACA 4065

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RESULT 10

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US-10-257-166-150/C
; Sequence 150, Application US/10257166
; Publication No. US20040023230A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Method and Nucleic Acids for Analysing the Methylation of
; TITLE OF INVENTION: Genes Implicated in Pharmacogenomics
; FILE REFERENCE: 5013.1011

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; CURRENT APPLICATION NUMBER: US/10/257,166
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: PCT/EP01/07470
; DE 10032529.7
; DE 10043826.1
; PRIOR FILING DATE: 2001-06-29
; 2000-06-30
; 2000-09-01
; NUMBER OF SEQ ID NOS: 178
; SEQ ID NO 150
; LENGTH: 8776
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-257-166-150

Query Match          58.4%; Score 29.8; DB 16; Length 8776;
Best Local Similarity 75.5%; Pred. No. 1.7;
Matches 37; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 TTTGCTACTGGCTGCGAGCTGAGCCGACCTCTTCTGCGACACATPAA 49
Db 3863 TTACTACTTAACCTACACATTAACCTTCTTCTCCACACATPAA 3815

RESULT 11
US-10-085-612-6
; Sequence 6, Application US/10085612
; Publication No. US20030096251A1
; GENERAL INFORMATION:
; APPLICANT: Guida, Marco
; APPLICANT: Hall, Jeff
; APPLICANT: Petros, William
; APPLICANT: Vredenburg, James
; APPLICANT: Colvin, Oliver
; APPLICANT: Marks, Jeffrey
; TITLE OF INVENTION: Methods for Evaluating the Ability to Metabolize Pharmaceuticals
; FILE REFERENCE: 4389-5-C1
; CURRENT APPLICATION NUMBER: US/10/085,612
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/144,367
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/271,630
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-612-6

Query Match          54.9%; Score 28; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTGCTACTGGCTGCGAGCTGAGCCCA 28
Db 7 TTGCTACTGGCTGCGAGCTGAGCCCA 34

RESULT 12
US-10-775-169-80/C
; Sequence 80, Application US/10775169
; Publication No. US20040175743A1
; GENERAL INFORMATION:
; APPLICANT: Wyech
; APPLICANT: Burczynski, Michael
; APPLICANT: Twine, Natalie
; APPLICANT: Dornier, Andrew
; APPLICANT: Trepicchio, William
```

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; TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
; FILE REFERENCE: AM101080 (031896-013000)
; CURRENT APPLICATION NUMBER: US/10/775,169
; CURRENT FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 5278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 80
; LENGTH: 4130
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-775-169-80

Query Match          53.3%; Score 27.2; DB 17; Length 4130;
Best Local Similarity 72.9%; Pred. No. 12;
Matches 35; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 1 TTTGCTACTGGCTGCGAGCTGAGCCGACCTCTTCTGCGACACATPAA 48
Db 2148 TTAAATGCTGGCCCGGAGCTTACGCCCATATTAATTATCATCATCA 2101

RESULT 13
US-09-764-891-8707/C
; Sequence 8707, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8707
; LENGTH: 8575
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-8707

Query Match          53.3%; Score 27.2; DB 10; Length 8575;
Best Local Similarity 72.9%; Pred. No. 13;
Matches 35; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 1 TTTGCTACTGGCTGCGAGCTGAGCCGACCTCTTCTGCGACACATPAA 48
Db 6589 TTAAATGCTGGCCCGGAGCTTACGCCCATATTAATTATCATCATCA 6542

RESULT 14
US-10-085-612-2
; Sequence 2, Application US/10085612
; Publication No. US20030096251A1
; GENERAL INFORMATION:
; APPLICANT: Guida, Marco
; APPLICANT: Hall, Jeff
; APPLICANT: Petros, William
; APPLICANT: Vredenburg, James
; APPLICANT: Colvin, Oliver
; APPLICANT: Marks, Jeffrey
; TITLE OF INVENTION: Methods for Evaluating the Ability to Metabolize Pharmaceuticals
; FILE REFERENCE: 4389-5-C1
; CURRENT APPLICATION NUMBER: US/10/085,612
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/144,367
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/271,630
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 34
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TYPE: DNA
ORGANISM: Homo sapiens
US-10-085-612-2

Query Match 52.9%; Score 27; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTGCTACTGCTGCAGCTGCAGCC 27
Db 7 TTTGCTACTGCTGCAGCTGCAGCC 33

RESULT 15
US-10-425-115-176951/C

Sequence 176951, Application US/10425115
Publication No. US20040214272A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

FILE REFERENCE: 38-21(53222)B

CURRENT APPLICATION NUMBER: US/10/425,115

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 176951

LENGTH: 704

TYPE: DNA

ORGANISM: Zea mays

FEATURE:

OTHER INFORMATION: Clone ID: MFT4577_92970C.1

US-10-425-115-176951

Query Match 52.2%; Score 26.6; DB 18; Length 704;
Best Local Similarity 78.0%; Pred. No. 17;
Matches 32; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 4 GCTACTGCTGCAGCTGCAGCCCTCTTCTGCAGC 44
Db 375 GCCACTGCTGCAGCTGCAGCCCTCTTCTGCAGC 335

Search completed: January 26, 2005, 19:49:31
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